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OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                             Result
  00000
                                                                                                         0.0
                                                                                                                                                                                                            o.
                                                                                                                                                                                                                                                                                                                                   score greater
                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                   ż
  38.6
38.6
34.2
33.4
33.2
33.2
33.2
33.2
                                                                                                                                                                                                                                                                                                             No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 November 6, 2002, 14:03:45; Search time 32.7914 Seconds (without alignments)
10995.308 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1736436 seqs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-833-740-7_COPY_1_210
                                                                                                                                                                                                            Match Length
                                                                                                                                                                                                                             Query
  29.6
18.4
18.3
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15.8
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                                                                                                                                                                                                                                                                                                                                                                                     0. /SIDSI/gcgdata/genesed/geneseqn-embl/NA1990.DAT: *
11. /SIDSI/gcgdata/genesed/geneseqn-embl/NA1990.DAT: *
22. /SIDSI/gcgdata/genesed/geneseqn-embl/NA1990.DAT: *
23. /SIDSI/gcgdata/genesed/geneseqn-embl/NA1991.DAT: *
24. /SIDSI/gcgdata/genesed/geneseqn-embl/NA1992.DAT: *
25. /SIDSI/gcgdata/genesed/geneseqn-embl/NA1993.DAT: *
26. /SIDSI/gcgdata/genesed/geneseqn-embl/NA1995.DAT: *
27. /SIDSI/gcgdata/genesed/geneseqn-embl/NA1995.DAT: *
28. /SIDSI/gcgdata/genesed/geneseqn-embl/NA1995.DAT: *
29. /SIDSI/gcgdata/genesed/geneseqn-embl/NA1997.DAT: *
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29. /SIDSI/gcgdata/genesed/geneseqn-embl/NA1999.DAT: *
29. /SIDSI/gcgdata/genesed/geneseqn-embl/NA20001A.DAT: *
29. /SIDSI/gcgdata/genesed/geneseqn-embl/NA2001B.DAT: *
29. /SIDSI/gcgdata/genesed/geneseqn-embl/NA2001B.DAT: *
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29. /SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT: *
29. /SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT: *
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                                                                                                     1612
13327
  496
1302
1732
1801
1838
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  ij
AAH43758
AAH04015
AAH15417
AAL07185
AAL07185
AAI60795
AAI59009
ABA83074
AAK94639
                                                                                                                                                                                                                                                                         SUMMARIES
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  Human polynucleoti
Human polynucleoti
Human transcriptio
Human full-length
                                                                                                                                                                                                              Description
                                                                                   Human reproductive
                                                                                                                             Human cDNA clone (
                                                                                                                                                                       5' flanking and 5'
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| DNA encouring Hover | AAS27823 | 22 | 16489 | 14.2 | | 45 |
|---------------------|----------|----|-------|----------|----------------|--------|
| se integr | AAZ34835 | 21 | 7958 | | 29.8 | 44 |
| - | AAV87950 | 20 | 670 | ٠. | | 43 |
| an | ABA08267 | 22 | 394 | ٠. | | 42 |
| | ABA18963 | 22 | 11713 | 14.3 | 30 | 41 |
| | ABA18962 | 22 | 11711 | 4. | 30 | 40 |
| Human reproductive | AAL04589 | 22 | 2073 | 4 | 30.2 | 39 |
| Ω | AAC35669 | 21 | 980 | 14.5 | 30.4 | 38 |
| Arabidopsis thalia | AAC48603 | 21 | 977 | • | 30.4 | 37 |
| | AAV09028 | 19 | 10529 | | 30.6 | ω 6 |
| . ລ | AAZ60231 | 21 | 4136 | 14.6 | 30.6 | ω 5 |
| kidney | AAX23521 | 20 | 16595 | 14.7 | 30.8 | 34 |
| Human immune/haema | AAK69248 | 22 | 4264 | 14.7 | 30.8 | ω |
| Human immune/haema | AAK69247 | 22 | 4264 | 14.7 | 30.8 | 32 |
| Human immune/haema | AAK68504 | 22 | 4264 | 14.7 | 30.8 | 31 |
| Human immune/haema | AAK68503 | 22 | 4264 | 14.7 | 30.8 | 30 |
| DNA encoding novel | AAS27636 | 22 | 4264 | 14.7 | 30.8 | 29 |
| DNA encoding novel | AAS27635 | 22 | 4264 | 14.7 | 30.8 | 28 |
| ` | AAK56984 | 22 | 555 | 14.7 | 30.8 | 27 |
| , cq | AAS27072 | 22 | 555 | 14.7 | 30.8 | 26 |
| | AAD00147 | 21 | 35414 | 14.8 | 31 | 25 |
| n reproductiv | AAL07075 | 22 | 9370 | 15.3 | 32.2 | 24 |
| Drosophila melanog | ABL21136 | 23 | 7632 | 15.4 | 32.4 | 23 |
| | ABL05570 | 23 | 4345 | 15.4 | 32.4 | 22 |
| - 1 | AAK94358 | 22 | 3464 | 15.4 | 32.4 | 21 |
| | ABL05802 | 23 | 3346 | 15.4 | 32.4 | 5 |
| | AAA94846 | 21 | 1285 | 15.4 | 32.4 | 9 |
| | ABL05803 | 23 | 1276 | | 32.4 | 30 . |
| | AAA72250 | 21 | 1194 | | 32.4 | 7 |
| ດນ | AAZ41329 | 20 | 1194 | | 32.4 | 91 |
| Human cDNA 3'-end | AAK92773 | 22 | 555 | | 32.4 | 5 |
| Drosophila melanog | AAA94801 | 21 | 553 | | 32.4 | 4 |
| Human reproductive | AAL04727 | 22 | 11360 | <u>ن</u> | 33.2 | ωi |
| Human reproductive | AAL03820 | 22 | 11360 | | 33.2 | |
| Human musculoskele | 65 | 22 | 7601 | 15.8 | ω (ω (| _ ; |
| Human musculoskele | AAL36532 | 22 | 7601 | | נו גי | 5 |

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0 0 0 0 0 0 0 0 0

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ALIGNMENTS

RESULT 1 AAH43758

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AAH43758 standard; DNA; 2170 BP

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5' flanking region; 5' UTR; untranslated region; murine; glucagon-like peptide-2; GLP-2; receptor; regulator; intestinal epithelium; lateral hypothalamus; promoter; d
                                                                                                                                                                                                                                    5' flanking and 5' UTR of GLP-2 receptor gene
                                                                                                                                                                                                                                                        30-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                             AAH43758;
                                                                                                                                                                         Mus musculus.
                                                                                                             misc_RNA
                                                                                                                                            misc_RNA
          25-OCT-2001.
                              WO200179290-A2.
                                                                                                                                            Location/Qualifiers 1656
                                                                                                             /note= "Punitive transcriptional start site" 1761..1763
                                                                      note= "Corresponds to
GLP-2R gene"
1875..1877
                                                   /note= "Putative translational start site"
                                                                                                     /*tag=
                                                                                                                                   /*tag=
                                                                                           translational start in rat/human
                                                                                                                                                                                               promoter; ds
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RESULT 2
AAH04015/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC This sequence represents the 5' flanking and 5' UTR of the murine CC glucagon-like peptide-2 (GLP-2) receptor gene. This sequence may be CC used in the DNA construct of the invention, such that it is linked CC for expression with a heterologous gene of interest. This construct CC is useful for screening compounds to identify regulators of GLP-2 CC receptor expression. The DNA construct is also useful for delivering CC a gene product to tissues selected from intestinal ppithelium and the CC lateral hypothalamus, by transfecting an organism, or a gametic or CC embryonic form of such an organism, with the construct. The DNA CC construct is also useful to identify cells capable of mediating CC expression from the chosen GLP-2R promoter, to identify regions of CC the GLP-2R promoter that are functional in a given cell type, and CC to screen for agents that modulate expression from the GLP-2R promoter. CC It can be used to map functional regions of the GLP-2R promoter. CC It can be used to map functional regions of the GLP-2R promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
07-FEB-2001
                              EP1074617-A2
                                                                                                 Human; primer;
                                                                                                                                Human cDNA clone (5'-primer) SEQ ID NO:850.
                                                                                                                                                                      26-JUN-2001
                                                                                                                                                                                                         AAH04015;
                                                                                                                                                                                                                                       AAH04015 standard;
                                                                                                                                                                                                                                                                                                                              1637
                                                                                                                                                                                                                                                                                                                                                                                                 1587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2170 BP; 574 A; 501 C; 550 G; 540 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant DNA construct, useful as drug screening tool and protein delivery vehicle, comprising glucagon-like peptide-2 recept gene, and linked to heterologous gene of interest for expression
                                                                                                                                                                                                                                                                                                                                         182 GCGTGGAGAGGATTTGTGCAAACATTTCC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drucker DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ONEO-) 1149336 ONTARIO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GCCTTGTTCTTCTCCTCAGCCTGTCAAGGAAGTCCCCAGAAAGCACAGCTGACTT-AGGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGGTCTGGGAAAAATCTCCCCAAGATTTTAGGAGGGGCAGGCGGGGGATGA----- 1586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCTTGCTTTTTCTTCTGGGCTTGCTGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGG 1535
                                                                                                                                                                                                                                                                                                                           GCCTGAAGAGGACTTGTGCAAACACTTCC 1665
                                                                                                                                                                                                                                                                                                                                                                                       -----GAAACTTGGAGATTCGGTAGATCGCTGTAGAGCAACTCAGACAGTC----GGCG 1636
                                                                                                                                                                                                                                                                                                                                                                                                                       GAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 1; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-196909P.
2001US-265310P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-IB00619
                                                                                        detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 62.2; DB 24; Pred No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
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AAH15417 sta AAH15417; 26-JUN-2001

(first entry)

standard; cDNA; 1612 BP

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RESULT 3
AAH15417/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary ct to the complementary strand of a polynucleotide which complementary ct the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of complementary strand of a polynucleotide which comprises a 5'-end cc complementary to a polynucleotide comprises a sequence complementary to a combination of complementary strand of a polynucleotide which comprises a 5'-end cc polynucleotide comprises a 3'-end sequence complementary to a combination of complementary to a complementary to
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 772 BP; 147 A; 258 C; 194 G; 170 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                138
                                                                                                                                   157 GACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAGGATTTGTGCA 201
                                                                                                                                                                                              198
                                                                                                                                                                                                                                                                                            258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 850; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-318749/34.
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                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                                         37
                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the present invention.
                                                                                                                                                                                                                                                                                  CCCAAGAAGCACAGGACCACCTGGGAAAGACAGGGGGACAGTCTCCCAGCCTGGGCACCCT 199
                                                                                                                                                                                                                                                                                                                             CACCTCATAGGGAAGACAGGCCTGATCCTGGTGAGGGTTTGCCCA
                                                                                                                                                                                      TAAATCTGGAGGAGGAAGCTCTTGCCTGGGGGAACATTACAGAGCCTGGAGCATAGGTTA 139
                                                                                                                                                                                                                                 CAGGGGGGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTA 156
                                                                                                                                                                                                                                                                                                                                                                                       86;
                                                                                                                                                                                                                                                                                                                                                                                                         n 18.4%;
Similarity 52.1%;
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                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0300253.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 38.6; DB Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 772;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000; 2000EP-0116126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of to the 5602 nucleotide sequences defined in the specification, where the the 5602 nucleotide sequences defined in the specification, where the complementary strand of a polynucleotide; or (b) a combination oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                            the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, in gene therapy. The primers are useful for synthesising polynucleotides, in gene therapy tull-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers allow obtaining of the full-length the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13639 represent human amino acid sequences; and AAH13629 to AAH13632 AAB95893 represent oligonucleotides, all of which are used in the exemplification represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a sequence and an oligonucleotide comprises a 3'-end sequence, where the polynucleotide which comprises a 1'-end sequence, where the onligonucleotide comprises at least 15 nucleotides and the combination of oligonucleotide comprises at least 15 nucleotides and those defined in the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; SEQ ID 13627; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                      Sequence 1612 BP; 352 A; 476 C; 391 G; 393 T; 0 other;
                                                                                                                                                                   258 CCCAAGAAGCACAGGACCACCTGGGAAAGACAGGGGACAGTCTCCCAGCCTGGGCACCCT 199
138 CACCTCATAGGGAAGACAGGCCTGATCCTGGTGAGGGTTTGCCCA 94
                                        157 GACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAGGATTTGTGCA 201
                                                                                                                                                                                                         37 CCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCCCTGCTTTTTGGGGGGG 96
                                                                                                                          97 CAGGGGCGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTA 156
                                                                                                                                                                                                                                                                             Local
                                                                                   TAAATCTGGAGGAAGCTCTTGCCTGGGGGAACATTACAGAGCCTGGAGCATAGGTTA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                   present invention.
                                                                                                                                                                                                                                                         86;
                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-0248036
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                                                                                                                                                                                                                                                                                18.4%; 52.1%;

 Mismatches

                                                                                                                                                                                                                                                                                  Score 38.6; DB 22; Length 1612; pred. No. 0.029;
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1 A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Otsuki T;
                                                                                                                                                                                                                                                                      79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto J;
                                                                                                                                                                                                                                                                           0;
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RESULT 4
AAL02939
AAL02939;
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                                                                                                                                                                                                                                                                                                          30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human reproductive system related antigen DNA SEQ ID NO: 5627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200155320-A2
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                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                    07-JUN-2000;
28-JUN-2000;
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17-MAR-2000;
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                                                                            22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
                                                                                                                                              18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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                                       06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                                             26-JUL-2000;
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                                                                      05-SEP-2000;
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2000US-0220964.
2000US-0224518.
2000US-0224513.
2000US-0225213.
2000US-0225214.
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2000US-0209467
2000US-0214886
2000US-0215135
2000US-0216847
2000US-0216880
2000US-0217487
2000US-0217487
2000US-0217487
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2000US-0184664.
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                                       2000US-0231242.
2000US-0231243.
2000US-0231243.
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                                                                                         2000US-0229345
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                                                                                                                         2000US-0228924
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2000US-0227182.
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  2000US-0232081
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AAL07185/c
ID AAL07185 standard; DNA; 496 BP
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           31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
    18-APR-2000;
                                                                                    17-JAN-2001; 2001WO-US01339
                                                                                                              02-AUG-2001.
                                                                                                                                   WO200155320-A2
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                           Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                   Human reproductive system related antigen DNA SEQ ID NO: 9873.
                                                                                                                                                                                                                               21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                           AAL07185;
                                                                                                                                                                                                                                                                                                                                                                  5824 TCATCAGAAGGACAAAGAAGCCAGGGAAACCTGGGGAGATGGGGGAGAGGACCAGGAAGAA 5883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13327 BP; 3096 A; 3875 C; 3799 G; 2557 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 5627; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is used in preventing, treating or ameliorating a medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding a reproductive system antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-465570/50.
                                                                                                                                                                                                                                                                                                                                               16 TCCTCAGCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                        60;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
; 2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0190874.
2000US-0190876.
2000US-0190876.
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0250391
2000US-0251030
2000US-025198
2000US-025191
2000US-0251479
2000US-0251856
2000US-0251869
2000US-0251989
2000US-0251989
2000US-0251989
2000US-0251989
2000US-0251989
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                                                                                                                                                                                                                                                                                                                                                                                                                               16.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 13327;
                                                                                                                                                                                                                                                                                                                                                                                                                43; Indels
                                                                                                                                                                                                                                                                                                                              5926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    condition
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0,

02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 13-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000;

2000US-023636 2000US-023636 2000US-023636 2000US-023637 2000US-023637 2000US-023703 2000US-023703 2000US-023703 2000US-023703 2000US-023703 2000US-023703 2000US-023993 2000US-0240960 2000US-0241785 2000US-0241785 2000US-0241806 2000US-0241806 2000US-0241806 2000US-0241806 2000US-0246475 2000US-0246475 2000US-0246476 2000US-0246476 2000US-0246478

29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

29-SEP-2000; 29-SEP-2000;

02-OCT-2000;

21-SEP-2000; 25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 27-SEP-2000;

2000US 0232399 2000US-0232400 2000US-0232401 2000US-0233063 2000US-0233064 2000US-0234274 2000US-0234274 2000US-0234274 2000US-0234998 2000US-0234998 2000US-0234984 2000US-0235884 2000US-02358836

08-NOV-2000

2000US-0246524 2000US-0246524 2000US-0246525 2000US-0246526 2000US-0246526 2000US-0246527 2000US-0246528 2000US-0246538 2000US-0246639

17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000 17-NOV-2000

2000US-0249216. 2000US-0249217. 2000US-0249218. 2000US-0249210. 2000US-0249211. 2000US-0249212.

2000US-0246610. 2000US-0246611. 2000US-0246613. 2000US-0249207. 2000US-0249208.

2000US-0249213.

2000US-0249244 2000US-0249245 2000US-0249264 2000US-0249265 2000US-0249297 2000US-0249299 2000US-0249299 2000US-0249309

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19-MAY-2000;
28-JUN-2000;
28-JUN-2000;
30-JUN-2000;
30-JUN-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-AUG-2000;
15-AUG-2000;
16-SEP-2000;
22-AUG-2000;
23-AUG-2000;
23-AUG-2000;
23-AUG-2000;
23-AUG-2000;
20-SEP-2000;
01-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
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14-SEP-2000;

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14-SEP-2000;

14-SEP-2000;

14-SEP-2000;

21-SEP-2000;

21-SEP-2000;

25-SEP-2000;

25-SEP-2000;

27-SEP-2000;

29-SEP-2000;

20-SEP-2000;

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2000US-0217487.
2000US-0218290.
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2000US-0224518.
2000US-0224519.
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2000US-0225213.
2000US-0225266.
2000US-0225266.
2000US-0225267.
2000US-0225267.
2000US-0225267.
2000US-0225270.
2000US-0225759.
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2000US-0209467.
2000US-0214886.
2000US-0215135.
2000US-0216647.
       2000US-0228934
2000US-0229343
2000US-0229343
2000US-0229343
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2000US-023396
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2000US-0233401
2000US-0233401
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2000US-0233463
2000US-0234584
2000US-023498
2000US-023498
2000US-0236869
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2000US-0226681.
2000US-0226868.
2000US-0227182.
2000US-0227009.
                             20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NO
number of human reproductive y--- in the prevention and treatment of reproductive system users in the prevention and treatment of reproductive system users including cancer. The present sequence is a genomic sequence encoding protein of the invention.
                                                                                                                               The
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                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                              Rosen CA,
                                                                                                                                                                                    Disclosure;
                                                                                                          present inve
                                                                                                                                                                                                                                                                                                              2001-465570/50.
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2000US-0241785.
2000US-0241786.
2000US-0241786.
2000US-0241808.
2000US-0241809.
2000US-0241826.
2000US-02418126.
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2000US-0246475.
2000US-0246476.
2000US-0246477.
2000US-0246524.
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2000US-0246526.
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2000US-0246532.
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2000US-0249218.
2000US-0249211.
2000US-0249214.
2000US-0249215.
2000US-0249214.
2000US-0249216.
2000US-0249214.
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2000US-0250160
2000US-0250391
2000US-0251390
2000US-0251988
2000US-0251479
2000US-0251856
2000US-0251856
2000US-0251869
2000US-0251869
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2000US-0251989
2000US-0251989
2000US-0251990
2000US-0259678
                                                                               invention provides the protein and coding sequences of uman reproductive system related antigens. These can be ention and treatment of reproductive system disorders,
                                                                                                                                                                                 SEQ ID NO
                                                                                                                                                                                       9873; 1297pp + Sequence Listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                      Wang J,
Zhao QA,
                                                                              Claim 1; SEQ ID NO 4784; 10078pp; English.
                                                                                                                                                                                                                                                                           03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                           Novel
                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                            09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                           26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                               WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                              19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 4784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI60795 standard; cDNA; 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 AAGCCAGTGCCATGAGTTTCGCGCACA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 GCAGCGTGGAGAGGATTTGTGCAAACA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 GCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 GGGGACATCAGGGAGACTGGAGACTACGCTGTTTGGTCCAGGCATAGGAGATGAGCCCTG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOCAT
                                                                                                                                                           2001-442253/47.
                                                                                                                 nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCGGGAAGGGACAGTGTGGATGGGCCAGGCGGAATCAGAGGGTTTCAGAGAAAGCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM41639
                                                                                                                                                                                   Wang Z, Zhou P,
                                                                                                         central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                      2000US-0552317
2000US-0598042
2000US-0620312
2000US-0653450
2000US-0662191
2000US-0662193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                               2000US-0727344
                                                                                                                                                                                                                                                                                                                                                   2000US-0488725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 69 A; 219 C; 108 G; 100 T; 0 other;
                                                                                                                                                                                                Asundi V,
Wehrman T,
                                                                                                                                                                                   Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.9%;
51.7%;
                                                                                                                                                                               Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33.4; DB Pred. No. 0.85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                           Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 496;
                                                                                                                                                                                          Zhang J;
                                                                                                                                                                                                        Ren F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                      Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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AAI59009/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                     09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                  P-PSDB;
                                                              WPI; 2001-442253/47.
                                                                                                               Tang YT,
                                                                                        Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                         numan; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; lentremmia.
                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                  29-NOV-2000;
                                                                                                                                                                               14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                           21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                 26-DEC-2000;
                                                                                                                                                                                                                                                                                                             26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                     WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO 1212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI59009 standard; cDNA; 1732 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, ActivinyInhibin activity, chemotractic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                      leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1302 BP; 275 A; 418 C; 357 G; 252 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                736 GCCGGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 GCCGAGAAGG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 47; Conserv
                                                  AAM39853
                                                                                    Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                       SS
                                                                                                                                                                                                    2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
                                                                                                                                                                            2000US-0662191
2000US-0693036
                                                                                                                                                                                                                                                                                   2000WO-US34263.
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                                                                                                                                                                  2000US-0727344
                                                                                             Asundi V, Chen R, Ma
Wehrman T, Xu C, Xue
                                                                                     Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.8%;
67.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33.2; DH
                                                                                   Drmanac RT;
                                                                                               Ma Y,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                               Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1302;
                                                                                                          Ren F,
                                                                                               Ç
                                                                                                        Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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such as central nervous

Novel nucleic acids and polypeptides, useful for treating disorders

system injuries

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful ingene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and spatial neuropathies and central neurous system diseases, such as localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activiny, chemotactic/chemokinetic activity, haemostatic activiny, activity, chemotactic/chemokinetic activity, drug screening, and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1212; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1732 BP; 372 A; 533 C; 443 G; 384 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification.
                                                                                                                                                                                                                                                                                                                                                                                              Human; transcription factor; TRFX; cell proliferative disease; autoimmune disease; inflammation; neurological disease; chromosome 13; developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV; neuroprotective; antiinflammatory; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human transcription factor TRFX-101 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA83074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA83074 standard; DNA; 1801 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               736
                                                                                                                                                                                                                                                                                                                                       WO200172777-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                         13-MAR-2000; 2000US-0188986
                                                                                                                                                                                                                                                                         13-MAR-2001; 2001WO-US08117.
                                                                                                                                                                                                                                                                                                        04-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 GCCGAGAAGG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 GGGAAGGTCTGGGAAAAATCTCCCTGCTTTTGGGGGGGCAGGGGCGGGGGGGATGAGCCAGG 118
                                              Novel transcription factor polypeptides, used to treat diseases associated with altered activity and expression of TRFX, and to
                                                                                                                                                                             Hillman JL,
                              for agents capable of modulating its activity
                                                                                            P-PSDB; ABB50250.
                                                                                                                                            Reddy R;
                                                                                                                                                             Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGGGAAGG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
                                                                                                               2001-570896/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                               Baughn MR,
Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.8%;
67.1%;
                                                                                                                                                               Tang
                                                                                                                                                                                Yue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33.2;
                                                                                                                                                                  YT,
                                                                                                                                                                  Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4;
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                                                                                                                                                                  Lu DAM,
P, Shah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Indels
                                                                                                                                                                    DAM, Patterson C;
Shah P, Au-Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1732;
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                                                             screen
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Claim 11; Pages 322-323; 327pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune/inflammatory, neurological and developmental disorders. A number of specific disorders/diseases are given in the specification, including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS, including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS, allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic allergies, anaemia, asthma, autoimmune thyroiditis, pancreatitis, grave's disease, multiple sclerosis, osteoarthritis, pancreatitis, coriasis, rheumatoid arthritis, systemic lupus crythematosus, ulcerative psoriasis, rheumatoid arthritis, systemic lupus crythematosus, ulcerative colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's disease, stroke, and viral, bacterial, fungal and protozoal infections. The present sequence maps to human chromosome 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the coding sequence for a human transcription factor. The transcription factor and its coding sequence are useful in the diagnosis, treatment and prevention of diseases associated with altered expression of the transcription factor e.g. cell proliferative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1801 BP; 387 A; 553 C; 474 G; 387 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human full-length cDNA, SEQ ID NO: 3613.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK94639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK94639 standard; cDNA; 1838 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                   08-JUL-1999; 99JP-0194486
11-JAN-2000; 2000JP-0118774
02-MAY-2000; 2000JP-0183765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1130094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 GCCGAGAAGG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              801 GCCGGGAAGG 792
The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by
                                                                                                                                                                                                                                                                                                   (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; 2000EP-0114089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID NO 3613; 1380pp + sequence listing; English
                                                                                                                                                         830 primers useful for synthesizing full length cDNA clones and their
                                                                                                                                                                                                                 WPI; 2001-524255/58.
                                                                                                                                                                                                                                                Wakamatsu A, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 15.8%;
Local Similarity 67.1%;
                                                                                                                                                                                              p-PSDB; AAM93696
                                                                                                                                          use in genetic manipulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
                                                                                                                                                                                                                                                                   Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                          99JP-0194486
                                                                                                                                                                                                                                                                     Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0:
                                                                                                                                                                                                                                                      Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33.2; Di
pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                          Hayashi K, I:
K, Kojima S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                              Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1801;
                                                                                                                                                                                                                                                             Otsuki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                              Kawai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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RESULT 10
AAL36532
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11-JUL-2000;
11-JUL-2000;
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Best Local
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30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2001; 2001WO-US01338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic: immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neuroprotections disorder; cardiovascular disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200155367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculoskeletal system; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human musculoskeletal system related polynucleotide SEQ ID NO 2897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL36532 standard; DNA; 7601 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1838 BP; 404 A; 565 C; 468 G; 401 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    756 GCCGGGAAGG 747
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1 Similarity 67.1%;
47; Conservation
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2000US-0216880
2000US-0217487
2000US-0217487
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2000US-0218290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection; human; secreted protein;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _DB 22; Length 1838;
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         14 - SEP - 2000
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25 - SEP - 2000
27 - SEP - 2000
29 - SEP - 2000
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02 - OCT - 2000
03 - OCT - 2000
04 - OCT - 2000
05 - OCT - 2000
06 - OCT - 2000
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23-AUG-2000;
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2000US-0225759.
2000US-0225759.
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08-NOV-2000;
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01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
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2000US-0249208.
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2000US-0249297.
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2000US-0246532.
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2001US-0259678.
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2000US-0250391.
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2000US-0251868.
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Barash SC,

2001-451937/48.

Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis

Example 2; SEQ ID NO 2897; 781pp + Sequence Listing; English

CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC for preventing, treating or ameliorating medical conditions e.g. by CC for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human CC tissues disclosed in the specification. The nucleic acids, proteins, CC antibodies and (anthagonists are useful in the diagnosis, treatment CC antibodies and (anthagonists are useful in the diagnosis, treatment CC discrease of the adrenal gland, bone, bone marrow, breast, CC discrease of the adrenal gland, bone, bone marrow, breast, CC discrease, alteract, liver, lung, or urogenital; (b) immune cC discrease, autoimmune thyroiditis, diabetes multitus, Crohn's disease, CC anaemia, autoimmune thyroiditis, diabetes multitus, Crohn's disease, CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound the color of the color of

parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direction with the sequences.

Sequence 7601 BP; 2275 A; 1450 C; 1551 G; 2325 T; 0 other;

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format directly
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RESULT 11
AAL36533
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6540 AACACT 6545
                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                                                                                                                                                                                                                04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human musculoskeletal system related polynucleotide SEQ ID NO 2898.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL36533 standard; DNA;
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30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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                                                                                                            26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                               WO200155367-A1
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                    19-MAY-2000;
                                                                                                                                                                                                                                                                                                    31-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                       18-APR-2000;
                                                                                14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 TTCTTTCTCCTCAGCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGAAATTATGGGTGTAATTGGAGTCACTGAAGGAGGAGTGGAGGCAGGAGCAGAAAA 6539
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                                                                                                                                                                                                         2000US-0198123.
2000US-0205515.
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2000US-0225759.
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2000US-0225213.
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                                                                       2000US-0225266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
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C for preventing, treating or ameliorating medical conditions e.g. by
C protein or gene therapy. The genes are isolated from a range of human
C tissues disclosed in the specification. The nucleic acids, proteins,
C antibodies and (antiagonists are useful in the diagnosis, treatment
C other cancers of the adrenal gland, bone, bone marrow, breast,
C astrointestinal tract, liver lung, or urogenital; (b) immune
C anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
C multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
C chealing; (e) neurological disease such as myocardial ischaemias; (d) wound
C and (f) infectious diseases such as viral, bacterial, fungal and
                       Query Match
Best Local
           Matches
                                                     Sequence 7601 BP; 2275 A; 1450 C; 1551 G; 2325 T; 0 other;
                                                                                           parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directions.
                                                                                                                                                                                                                                                                                                                 The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
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06-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 2898; 781pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                 y Match 15.8%;
Local Similarity 54.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
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17-NOV-2000;
       68; Conservative
                                                                                  pecification, but was obtained in electronic format directly
at ftp.wipo.int/pub/published_pct_sequences.
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Gaps
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AAL03820/c
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18 - AUG - 2000;

22 - AUG - 2000;

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01 - SEP - 2000;
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14 - AUG - 2000;
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07-JUL-2000;
07-JUL-2000;
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19-MAY-2000;
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4760 GCCGGGAAGG 4751
                               Homo sapiens.
                                                       cancer;
                                                                                   Human reproductive system related antigen DNA SEQ ID NO: 7415.
                                                                                                             21-NOV-2001 (first entry)
                                                                                                                                        AAL04727;
                                                                                                                                                          AAL04727 standard; DNA; 11360 BP.
                                                                                                                                                                                                                                                              Sequence 11360 BP; 2899 A; 2709 C; 2708 G; 3044 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 6508; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                                                                                                                                                    reproductive system related antigen; reproductive system disorder; gene therapy; ds.
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67.1%;
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Pred. No. 2.6;
0; Mismatches 23; Indels 0;
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30-JUN-2000;
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14-JUL-2000;
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04-EB-2000;
24-EB-2000;
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16-MAR-2000;
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2000US-0190076.
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Rosen CA,

Barash SC,

Ruben SM;

understanding of the link between odour recognition and behaviour in

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Odorant receptor; fruit fly; DOR62; odour recognition; pest control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster odorant receptor DOR62 coding sequence.
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The present sequence is the coding sequence for the Drosophila melanogaster odorant receptor DOR62. It was isolated using a differential cloning strategy. The odorant genes and proteins are useful as they aid in the study of the olfactory organ in mammals, as well as aiding the
                                                                                                                             Novel nucleic acid encoding an insect odorant receptor, for identi modulator compounds that are useful in controlling pest population
                                                                                                                                                                                                                                                                                                                                                 25-FEB-2000; 2000WO-US04995
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                                                                                                                                                                                                                                                                                                                                                                                                                       WO200050566-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                          Claim 4; Fig 8; 176pp; English.
                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                       WPI; 2000-572081/53.
                                                                                                                                                                                                                                         Vosshall LB,
                                                                                                                                                                                                                                                                                                               25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                             COLUMBIA NEW YORK.
                                                                                                                                                                                                                                         Amrein HO,
                                                                                                                                                                                                                                                                                                               99US-0257706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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RESULT 15
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily
                                                                                                                                   Claim 3; SEQ ID NO 1233; 1380pp + sequence listing; English
                                                                                                                                                                             830 Primers useful for synthesizing full length cDNA clones
                                                                                                                                                                                                                                                                                                                                     08-JUL-1999;
11-JAN-2000;
                                                                                                                                                                       use in genetic manipulation
                                                                                                                                                                                                                   WPI; 2001-524255/58.
                                                                                                                                                                                                                                                 Wakamatsu A,
                                                                                                                                                                                                                                                                  Ota T,
                                                                                                                                                                                                                                                                                           (HELI-) HELIX RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1130094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA 3'-end sequence, SEQ ID NO: 1233.
                                                                                                                                                                                                                                                                                                                                                                                                               05-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 553 BP; 141 A; 145 C; 132 G; 135 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptors associated with fertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 GTACAGGAAGTGCATGGCGACGGTACACTGGACGGCGGCGGAGCAGACGAACTGGGCCAT 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 CGCCTCGCTCTGTGTCCGCATCCTGTCCCCAAAATAGCAGATTACAAACACCTCCAAGGT 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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2000JP-0118774.
2000JP-0183765.
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Nagai K, Kojima S,
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
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T, Koga H;
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                                                                                                                                                                                                                                                                                                                                                                                                                     without any special methods. The present sequence is the nucleotide sequence of the 3'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 555 BP; 124 A; 148 C; 167 G; 110 T; 6 other;
                                                                    205 GCCCCTTAGTGAGGTGTCACCTCTCCCAGAGTCACAGGACGCTTCTGGGA
                                                                                                                                            145 CCCCAGATGTAGGGGAGGCCTGATTCGCATCGGGGCCGGGCGCGTTACTCCATGGGGTCG
                                                                                                                                                                                                                                                            19 TCAGCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATC 78
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                                                                                                       ACTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGCAGCGTGGA 188
                                                                                                                                                                                 TCCCTGCTTTTGGGGGGGGAGGGGGGGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAG 138
                                                                                                                                                                                                                         TTAACCTGAATTTAAAAGCACACGAAACAAAGGTGTCAATGGGAATCTCGCGGCCAACGC 144
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OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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            вн106958
вн113183
                                 AZ408884
CNS05CP4
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AL175958 Tetraodon
AA422680 vd29d10.s
AZ406458 1M0175007
B1844815 fq14c10.x
AL515339 AL515339
AL249035 Tetraodon
AZ40884 1M0180D22
AL331393 Tetraodon
BH106958 RPCI-24-2
BH113183 RPCI-24-2
BH113183 RPCI-24-2
AZ256572 RPCI-23-1
                                                                                                                       AZ971837 2M0245B02
AL258341 Tetraodon
AL196781 Tetraodon
AZ463187 1M0271B21
AL233144 Tetraodon
AZ394294 1M0157J18
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | ω 5 | 34 | 3 3 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | |
| 62 | 62.2 | 1.3 | N1 | N) | K) | N) | K1 | N) | K) | 62.6 | K) | N | N | N | N | 63 | 63 | 63 | ω | w | w | ω | w | 63.4 | • | 63.6 | ω | |
| 3.7 | 3.7 | | | | | | | | | | | | | | | | | | | ٠ | | | • | | 3.8 | 3. 8 | | |
| 294 | 1100 | 764 | 666 | 625 | 437 | 426 | 922 | 783 | 852 | 489 | 945 | 858 | 817 | 811 | 602 | 813 | 415 | 383 | 772 | 640 | 613 | 473 | 871 | 813 | 437 | 598 | 491 | |
| | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 12 | 10 | 10 | 12 | 12 | 2 | 12 | 12 | 12 | 12 | 12 | 10 | 12 | |
| AA078583 | CNS05DQZ | AZ332426 | AZ967532 | CNS03FZH | вн320813 | AZ435066 | CNS05HKN | CNS04G1P | CNS0300G | AZ101812 | CNS02H50 | CNS041WD | CNS053B9 | вн315615 | AZ340230 | BG069448 | W54246 | BH097540 | AZ783123 | AZ377122 | AZ222674 | CNS02TK6 | CNS05IR1 | CNS03XZZ | FR0008122 | BM156047 | AZ902149 | |
| AA078583 7P05H08 C | AL332756 Tetraodon | AZ332426 1M0060122 | AZ967532 2M0238F05 | AL242342 Tetraodon | вн320813 Сн230-159 | 1M0221K0 | | AL289078 Tetraodon | | AZ101812 RPCI-23-2 | | AL270742 Tetraodon | AL319230 Tetraodon | вн315615 СН230-12J | | | | BH097540 RPCI-24-2 | | | | | AL339238 Tetraodon | | z91932 F.rubripes | 7 | AZ902149 RPCI-24-1 | |

ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS LOCUS DEFINITION RESULT 1 AZ971837/c FEATURES COMMENT TITLE ORGANISM JOURNAL source AZ971837 689 bp DNA linear GSS 27-APR-200 2M0245B02R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0245B02 R, DNA sequence. Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0245 row: B column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 to 689)
1 (bases 1 to 689)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rei University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Res 84112, USA Unpublished (2000) Contact: Robert B. ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A AZ971837 High quality sequence stop: 689 plasmid inserts Mouse whole genome scaffolding with paired end reads from 10kb Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mus musculus AZ971837.1 nouse mouse /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="ftaxon:10090"
/clone="UUGC2M0245B02"
/clone_lib="Mouse 10kb plasmid UUGC2M library" Location/Qualifiers GI:13843064 . 689 Weiss Polymers Research Bldg., 20 Pedersen, T., Reilly çs 2030 GSS 27-APR-2001 EI . SLC, T

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Query Match
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                                                                                                                                                                                                                                                                                                CCATCCTCTCCAGCCATCCGAATCTCAATCTGGTCGTGTGCGTAAGAATAGAATCCTCGG 1463
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TGAGAAACTTG 1594
                                                                                ACGTCTTGGGGGTAGGTCTGGGAAAAATCTCCCCAAGATTTTAGGAGGGGCAGGCGGGGGA 1583
                                                                                                                                                                                                            AATGGTAACCATGTCTTGCTTTTTCTTCTGGGCTTGCTGAGGAAGTCCCCAGGCAGCGTAG 1523
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                                                       ACGTCTTGGGGGTAGGTCTGGGAAAAATCTCCCAAGATTTTAGGAGGGGCAGGCGGGGGA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
189 c 147 g 180 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory Mouse DNA Resource
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Pred. No. 4.2e-134;
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ORIGIN BASE COUNT

Matches

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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 138G22 of library G from Tetraodon nigroviridis, genomic survey

681 bp

DNA

linear

GSS 13-MAY-2000

CNS02GTW

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1404

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1284

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REFERENCE
AUTHORS
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                                        ACACATGTTTTCTTCCCTCC 294
                                                                                   GCTGCTCTGTCCACCGCCAGCCTGGCTTCAATCAGCCCCAGGAACGTGTGAGGRGGKCCA 766
                                                                                                                                                                                                                GGTGCTTTCTCCCCCACCATGCGACCCGGGAGCTCCACTGATATGGACAGAATAGCTTTA 214
ACTCATGAGGTCATCCCTCC
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS; genome survey sequence Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. Weissenbach,J.
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Tetraodon nigroviridis genome survey sequence T7 end of clone
051G20 of library G from Tetraodon nigroviridis, genomic survey
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st-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                       191
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                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                         /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="051620"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG051BD10LP1-end : T7"
/note="Genoscope sequence ID : C0BG051BD10LP1-end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Pred. No. 5.5e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTCCCTCCACTTCCTCCCATTCTCTGTGGTCC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
AL196781
AL196781.1 GI:7834931
AL196781.1 GI:7834931
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                  AZ463187

511 bp DNA linear GSS U4-UCT-200
1M0271B21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0271B21 R, DNA sequence.
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Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 511)
                                                                                                                                                                                                                          AZ463187
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                                                                                                                                          Mus musculus
                                                                                                                                                                                  AZ463187.1 GI:10621312
GSS.
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/db_xref="taxon:99883"
/clone="138G22"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0271 row: B column: 21
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                 Tetraodon
006A06 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92;
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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Contact: Robert B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732141gb) her129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and nurified The characted adaptors to the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance. Table 165 c 78 g 129 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA
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/db_xref="taxon:10090"
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library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 684)
                                                                                                                                                 Mus musculus
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AZ394294
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Roest-Crollius, H., Jaillon, O.,
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/note="Genoscope sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="006A06"
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Pred. No. 0.00066;
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n, W., Bernot, A.
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155 GGTGCTTTCTCCCCCACCATGCGACCCGGGAGCTCCACTGATATGGACAGAATAGCTTTA 214
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                                                                                                                                                                                                                                                                                                                                                                                                              GGTTCAATCTCTAGTACAACATAAACTGGGACATACAAGACTTTGTCTCAAAGAGCTAAA 204
GSS; genome survey sequence. Tetraodon nigroviridis.
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Unpublished (2000)
Contact: Robert B.
                                                    AL175958.1 GI:7814015
                                                                                                      sequence.
                                                                                                                             Tetraodon
224G15 of
                                                                                                                                                                                  CNS020RH
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0157 row: J column: 1
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Fax: 801 585 7177
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University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                             nigroviridis genome surve
library G from Tetraodon
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/clone="UUGC1M0157J18"
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Pred. No. 0.00073;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 729)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fis Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. Weissenbach, J.
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                                                                                                                                                                                                        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA422680
398 bp
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IMAGE: 793939 5', mRNA sequence.
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Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charaterization and repeat analysis of the compact genome of the
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                                                       Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 398)
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Washington University School of MedicineP
                                WashU-HHMI Mouse EST Project
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/db_xref="taxon:99883"
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72.8%;
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Pred. No. 0.00073;
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353 CACA 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87;
                                                                                                          Contact: Robert B. University of Utah University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                Dunn, D., Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1M0175007\ensuremath{R} Mouse 10\ensuremath{\text{kb}} plasmid UUGClM library Mus musculus genomic clone UUGClM0175007 R, DNA sequence.
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                       Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads
                                                                                                                                                                                                                                                  and Wright, D., Weiss, R
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                     ISlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse
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                                                                                                                                                                                                     inserts
                                                                                          Biomedical Polymers Research Bldg.,
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/tissue_type="embryo"
/dev_stage="2-cell"
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/db_xref="taxon:10090"
/clone="IMAGE:793939"
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70.2%;
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                                                                                                                                                            Weiss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 0.0009;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            fq14c10.x1 zebrafish adult brain Danio rerio cDNA clone 4831482 3' similar to TR:09UMF8 O9UMF8 TRANSALDOLASE; contains element MER35 repetitive element; mRNA sequence.
  Unpublished (1998)
Contact: Stephen L
                                                 WashU Zebrafish EST Project 1998
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                           and Wilson, R
                                                                                             Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R
                                                                                                                                                                                                                                                                                                                                   Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                               BI844815.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Stephen L.
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/note="Vector: PW042nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone="UUGC1M0175007"
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/strain="C57BL/6J"
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AL515339
                                                                                                                                                                                                                Unpublished (2001)
Contact: Genoscope
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BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                          Li, W.B., Gruber, C., Jessee, J. a
Full-length cDNA libraries and
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 589)
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/note="Vector: pZIPLOX; Site_1: Not1; Site_2: Sall;
Original library was constructed in lambdaZIPLOX. Nexcision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."

152 c 98 g 107 t 1 others
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                            /clone="CL0BB029ZG08"
                                                                                                                                Location/Qualifiers
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/dev_stage="adult"
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/clone="4831482"
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/sex="mixed male and female"
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82.2%;
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Pred. No. 0.0011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei, Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                               Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon nigroviridis genome survey sequence T7 end of clone 034P14 of library G from Tetraodon nigroviridis
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                   /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="034P14"
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157 c 16 g 150 t 2:
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/clone_lib="G"
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ANAORRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0180 row: P column: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Utah Genome University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ408884.1 GI:10532897
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                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected
                                                                                                                                            Laboratory Mouse DNA Resource
                                                                                                                                                             /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0180P22"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Genoscope sequence ID : C0BG034DH07LP1~end : T7" 274 c 246 g 221 t 3 others
                                                                                                                                                                                                                        /sex="Male"
                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.9%;
66.7%;
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Pred. No. 0.0011;
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  for a 9.5
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RESULT 14
CNS05CP4
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ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACAGCATTCTTGTTACATCATATGTCTTCAGTGGTATCTCTGTTTTCTTCAAATATCCC 355
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                                                                                                                                                                           Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                        Human gene number estimate provided by genome Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 957)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Boune
Bernot,A., Fizames,C., Wincker,P., Brottler,P.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Charaterization and repeat analysis of the c
freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS; genome survey sequence Tetraodon nigroviridis.
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                                                                                                                                                      http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                      Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weissenbach,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roest-Crollius, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodontidae;
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                                           /organism="Tetraodon nigroviridis'
/db_xref="taxon:99883"
/clone="020P23"
/note="Genoscope sequence ID : COAA020CH12A2~end : T3"
                         /clone_lib="A"
                                                                                                                                    Location/Qualifiers
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64.48;
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Pred. No. 0.0012;
""" amatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On,O., Dasilva,C., Fiza
Quetier,F., Saurin,W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    compact
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                                                                                                                                                                                                                                                                                                                                                                             wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                        Quetier, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bernot, A.
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RESULT 15
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Best Local
                                                              Matches
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                                                                              Best
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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483
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TGTTCTCTTTAGAACTCGTCTCATCCTCCCTGGNAGCTATGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68;
                                                                                                                                                                                                                                                                                                                                                                                                            Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library PAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC or
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 264 row: G column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao,S., Nierman,W., Malek,J., Shatsman,S., Al
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPCI-24-264G24.TV RPCI-24 Mus musculus genomic clone RPCI-24-264G24
                                                                                                                                                                                                                                                                                                                                                                                Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1, (bases 1 to 484)
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                                                              Conservative
                                                                                                                                           D
                                                                                                                                                      /note="Yector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="RPCI-24-264G24"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                   . .484
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                           3.8%;
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75.2%;
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                                                                                    Glp-2 receptor gene promoter and uses thereof Patent: WO 0179290-A 7 25-OCT-2001; 1149336 ONTARIO INC. (CA)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                           Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 26, 2001 this sequence version replaced gi:14547870. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 198271).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                               Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 17, clone RP11-655D3
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           (bases 1 to 198271)
Center project
                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                            Center code: WIBR
                                                                                                                                                                                                                  A.F.A. & Green, P. (1996-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ordered pieces.
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SEQUENCING
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RESULT 3
AC087646/c
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AUTHORS
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TITLE
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les 210; Conserv
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S. Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dlaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            210719 bp DNA linear H
Homo sapiens chromosome 17 clone RP11-773021 map 17,
SEQUENCE, 12 unordered pieces.
                                                                                                                                                                          Homo sapiens chromosome 17, clone RP11-773021
Unpublished
                                                                                                                                                                                                                      1 (bases 1 to 210719)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                             Homo sapiens
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1 153566: contig of 153566 bp in length 153567 153666: gap of 100 bp 153667 158888: contig of 5222 bp in length 158989 158988: gap of 100 bp 158989 189474: contig of 30486 bp in length 189475 189574: gap of 100 bp 189475 189574: gap of 100 bp 189575 198271: contig of 8697 bp in length.
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45543 c 46237 g 53270 t 363 others
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/chromosome="17"
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Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,
Marquis, M., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,
McCheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
McCheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
McConnor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Phunkhang, P., Pierre, N., Pollara, V., Rognond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, M., Subramanian, A., Talamas, J., Tesfayers, Theodore, J.,
Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Tember I., Timana, J., Tey, M., J., Young, G., Zainoun, J.,
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Jones,C., Karatas,A.,
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75255 75354: gap of 100 bp
75355 76881: contig of 1527 bp in length
76882 76981: gap of 100 bp
76982 78538: contig of 1557 bp in length
78539 78638: gap of 100 bp
78639 79946: contig of 1570 bp in length
78639 79946: contig of 1308 bp in length
79947 80046: gap of 100 bp
82098 contig of 2052 bp in length
82099 82198: gap of 100 bp
82199 86309: contig of 4111 bp in length
83110 86409: gap of 100 bp
86410 88601: contig of 4111 bp in length
86310 86409: gap of 100 bp
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Consensus quality: 205962 bases at least Q40 consensus quality: 208431 bases at least Q30 Consensus quality: 208431 bases at least Q30 Consensus quality: 209109 bases at least Q20
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Insert size: 209619; sum-of-contigs
Quality coverage: 8.4 in Q20 bases; agarose-fp
Quality coverage: 8.2 in Q20 bases; sum-of-contigs
                                                                            121202
154072
154172
                                                                                                                                    105001 105100: gap of 100 up
105101 121101: contig of 16001
121102 121201: gap of 100 bp
121202 154071: contig of 32870
100 bp
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Center clone name: 773_0_21
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                                                                                                                                                                                                                                                                                                               86410 89601: contig of 3192 bp in length
89602 89701: gap of 100 bp
89702 105000: contig of 15299 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                             86310 86409:
86410 8960
154171: gap of 100 bp
19398: contig of 39814 bp in length
194085: gap of 100 bp
210719: contig of 16634 bp in length
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121101: contig of 16001 bp in length
1201: gap of 100 bp
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                                                                                                                                                         bp in length
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COMMENT

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                                                     ORGANISM
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                                                                                                                                        AC069006 213359 bp DNA linear HTG 11-DEC-20 Homo sapiens chromosome RPCI-11 clone RP11-773021, WORKING DRAFT SEQUENCE, 16 unordered pieces.
1 (bases 1 to 213359)
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                   Homo sapiens
                                                                                                                           AC069006
                                                                                                         AC069006.4 GI:11612641
                                                                                        HTG; HTGS_PHASE1; HTGS_DRAFT
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80047. 82009
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89702. .105000
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154172. .193985
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121202. .154071
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105101. .121101
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/db_xref="taxon:9606"
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               source
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Insert size: 211859; sum-of-contigs
Quality coverage: 5.34 in Q20 bases; agarose-fp
Quality coverage: 5.44 in Q20 bases; sum-of-contigs
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Submitted (16-MAY-2000) Genome Sequencing Center, Washington Submitted (2000) of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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∕organism≔"Homo sapiens"
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117462: contig
117562: gap of
143519: contig
143619: gap of
                                            143619: gap of unknown length
171176: contig of 27557 bp in
171276: gap of unknown length
213359: contig of 42083 bp in
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171277. .213359
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143620. .171176
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94748. .117462
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78637. .94647
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10515. .53087
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/note="assembly_name:Contig20"
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/chromosome="RPCI-11"
/clone="RP11-773021"
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                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (17-JAN-2001) Department of Medicine, University of
Toronto, 101 College Street CCRW3-845, Toronto, ON M5G2C4, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                              Lovshin, J.A., Estali, J., Yusta, B., Brown, T.J. and Drucker, D.J. Glucagon-like Peptide (GLP)-2 Action in the Murine Central Nervous System Is Enhanced by Elimination of GLP-1 Receptor Signaling J. Biol. Chem. 276 (24), 21489-21499 (2001)
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/db_xref="taxon:32630"
                                                                                                                                   /product="glucagon-like peptide-2 receptor" 2835. .>2900
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                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="129/SvJ"
/db_xref="taxon:10090"
                                  /product="glucagon-like peptide-2 receptor"
/protein_id="AAK63043.1"
/db_xref="GI:14485647"
                    translation="MRRLWGPGTPFLSLLLLVSIKQ"/
                                                                                              /codon_start=1
                                                                                                                 /note="GLP-2 receptor"
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                                                                                                                                                                                                                                                                                                                                                                    Submitted (30-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 1, 2000 this sequence version replaced gi:6970326.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus chromosome 11, clone RP23-409J21
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                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
Assembly program: Phrap; version 0.960731
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67.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3130;
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NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the cohtigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 196848 bases at least consensus quality: 202204 bases at least Consensus quality: 202202 bases at least Insert size: 210000; agarose-fp Insert size: 205160; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                 149263 149362: gap of 100 bp 1149263 175777: contig of 28215 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                    115974 116073: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 4.8 in Q20 bases; agarose-fp Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                        116074
                                                                                                                                                                                                                                                                                                                                       177578 177677: gap of
                                                                                                                                                                                                                                                                                                                                                                                              132295 132394: gap of 132395 149262: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88149 88248:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25639
31996 32095:
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40234 482
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10638 14144: contig of 3507 b
14145 14244: gap of 100 bp
14245 18479: contig of 4235 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75457 75556:
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1960 4152: contig of 2193 bp in length
4153 4252: gap of 100 bp
4253 6291: contig of 2039 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 641: gap of
                                  1960
                                                                                                        clone_end:T7
          /note="assembly_fragment"
                                              note-"assembly_fragment"
                                                                                  vector_side:right"
                                                                                                                                                              /clone="RP23-409J21"
/clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                        note-"assembly_fragment
                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                         /chromosome="11"
                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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63846: contig of 8395 bp in length
63946: gap of 100 bp
75456: contig of 11510 bp in length
75556: gap of 100 bp
88148: contig of 12592 bp in length
88248: gap of 100 bp
99481: contig of 12592 bp in length
99581: gap of 100 bp
99581: gap of 100 bp
115973: contig of 16392 bp in length
115973: contig of 16392 bp in length
                                                                                                                                                                                                                                                                                                                 767/: gap of 100 bp
207160: contig of 29483 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8579: gap of 100 bp
25538: contig of 6959 bp
5638: gap of 100 bp
31995: contig of 6357 bp
2095: gap of 100 bp
40133: contig of 8038 bp
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10537: contig of 4146 bp in length
                                                                      1859
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contig of 16868 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                              ap of 100 bp contig of 16221 bp in length
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contig of 6987 b
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                                            SOURCE
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                        ORGANISM
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Best Local Similarity
                                                                                                                                                                                                                                                   28834 GCCTGAAGAGGACTTGTGCAAACACTTCC 28862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28673 GTCTTGCTTTTTCTTCTGGGCTTGCTGAGGAAGTCCCCAGGCAGCGTAGACGTCTTGGGGG 28732
                                                                                                                                                                                                                                                                                                                           28784 -----GAAACTTGGAGATTCGGTAGATCGCTGTAGAGCAACTCAGACAGTC----GGCG 28833
                                                                                                                                                                                                                                                                                                                                                                                                        28733 TAGGTCTGGGAAAAATCTCCCAAGATTTTAGGAGGGGCAGGCGGGGGATGA------
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                                                                                                                                                                                                                                                                                                                                                                                                                              62 AAGGTCTGGGAAAAATCTCCCCTGCTTTTGGGGGGGGCAGGGGCGGGGGGATGAGCCAGGGCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GCCTTGTTCTTCTCCTCAGCCTGTCAAGGAAGTCCCCAGAAAGCACAGCTGACTT-AGGG 61
                                                                                                                                                                                                                                                                                           GCGTGGAGAGGATTTGTGCAAACATTTCC 210
                                                                                                              AL646097 211173 bp DNA 1.
Mus musculus chromosome 11 clone RP23-338M9,
PROGRESS ***, in unordered pieces.
                      Mus musculus
                                                      HTG; HTGS_PHASE1; HTGS_DRAFT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                            AL646097.5 GI:18135259
                                                                                                  AL646097
                                            house mouse.
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177678. .207160

/note="assembly_fragment"
/ 46293 c 45874 g 55300
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88249. .99481
/note="assembly_fragment"
99582. .115973
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149363. .177577
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6392. .10537
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32096, .40133
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67.5%;
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FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: XGAP4, version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 207636 bases at least Q40
Consensus quality: 207698 bases at least Q20
Consensus quality: 208567 bases at least Q20
Consensus quality: 208567 bases at least Q20
Insert size: 209573; sum-of-contigs
Insert size: 207120; 2.8% error; agarose-fp
Quality coverage: 9.05x in Q20 bases; sum-of-contigs Quality
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----- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved
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/chromosome="11"
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fragment_chain:1"
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fragment_chain:2"
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fragment_chain:2"
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fragment_chain:1"
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fragment_chain:2"
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fragment_chain:2"
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fragment_chain:2"
/note="assembly_fragment:00072
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Db 132359 GTCTTGCTTTTTCTTCTGGGCTTGCTGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGG 132300
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AX354812
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                                                                                                                                                                                                                                                                                                                                                                                                                         493 bp
Sequence 6 from Patent W00179290.
AX354812
                                                                                                                                                                                                                                            Glp-2 receptor gene promoter and uses thereof patent: WO 0179290-A 6 25-OCT-2001; 1149336 ONTARIO INC. (CA)
                                                                                                                                                                                                                                                                                                                                                                                                           AX354812.1 GI:18619543
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                             Drucker, D.J. and Lovshin, J.A.
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146293. .185554
/note="assembly_fragment:01439
fragment_chain:2"
nosess
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201054. 211173
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195532. .200953
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fragment_chain:2"
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fragment_chain:2
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                                                                  /translation="MRRLWGPGTPFLSLLLLVSIKQ"
132 c 155 g 104 t 2 ot
                                                                                                 /protein_id="CAD22992.1"
/db_xref="GI:18619544"
                                                                                                                                              /note="unnamed protein product"
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                                                                                                                                                                                               organism="Mus sp."
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      Score 54; DB 6;
Pred. No. 6.3e-06;
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BASE COUNT
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                                                                                 96;
                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission

Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Telisl-1438-52-3951, Fax:81-438-52-3952)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library Construction, 5'-6 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mlshikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T. NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oligo capping; fis (full insert sequence). Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to mRNA, clone_lib:HEMBA1 clone:HEMBA1005931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
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                                                                                                                                                                                                   352
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Ogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T.,
                                                                       Conservative
                                                                                                                                                                        /dev_stage="embryo, 10 weeks"
/tissue_type="whole embryo, mainly head"
/note="cioning vector: pME18SFL3"
/note="cioning vector: pME18SFL3"
/note="cioning vector: pME18SFL3"
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                                                                                                                                                                                                                                                                                  /clone="HEMBA1005931"
/clone_lib="HEMBA1"
                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                      18.4%; Score 38.6; DB 9; 52.1%; Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 GACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAGGATTTGTGCA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 TAAATCTGGAGGAAGCTCTTGCCTGGGGGAACATTACAGAGCCTGGAGCATAGGTTA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 CCCAAGAAGCACAAGGACCACCTGGGAAAGACAGGGGGACAGTCTCCCAGCCTGGGCACCCT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 CAGGGGCGGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 202251 bases at least 240
Consensus quality: 202335 bases at least 230
Consensus quality: 202396 bases at least 220
Insert size: 202482; sum-of-contigs
Insert size: 198528; 5.3% error; agarose-fp
Quality coverage: 10.24x in 220 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Feb 1, 2002 this sequence version replaced g1:17384473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: bA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: humquery@sanger.ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matthews, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202682 bp DNA linear HTG 30-
HOMO sapiens chromosome 1 clone RP11-415J8, *** SEQUENCING
PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                  be preserved.
                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL513327.22 GI:18476646
                                                                                                                                                                                                                       53968 54067: gap of 100 bp
54068 147217: contig of 93150 bp in length
147218 147317: gap of 100 bp
147318 202682: contig of 55365 bp in length
                                                                                                                                                                                                                                                                             1 53967: contig of 53967 bp in length 54068 147217.
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/note="assembly_fragment:03338
fragment_chain:1"
                                                                  /clone_lib="RPCI-11.2"
                                                                                           /clone="RP11-415J8"
                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                           /organism="Homo sapiens"
                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk
                                                                                                                                                                                      .202682
                                              . 53967
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RESULT 12
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78643 CACCTCATAGGGAAGACAGGCCTGATCCTGGTGAGGGTTTGCCCA 78599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78703 TAAATCTGGAGGAAGCTCTTGCCTGGGGGAACATTACAGAGCCTGGAGCATAGGTTA 78644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78763 CCCAAGAAGCACCACCACCTGGGAAAGACAGGGGACAGTCTCCCAGCCTGGGCACCCT 78704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGGGCGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbarla,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cheveland,C.D., Cox,C., Chen,Z., Chowdhry,I., Christopoulos,C., Cheveland,C.D., Cox,C., Chen,Z., Chen, C., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus clone CH230-160H18, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Norway rat.
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Stone, H., Sutton, A., Svatek, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
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fragment_chain:1"
a 47427 c 48564 g 54202 t
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147318. .202682
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/note="assembly_fragment:06038
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52.1%;
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           Tamerisa, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 75 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-----Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Lario, P., Lee-Lin, S.-O., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                    Submitted (21-SEP-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC096681 145617 bp DNA linear HTG 21-Canis familiaris clone RP81-228C19, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity 59.6 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Green, E.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1. (bases 1 to 145617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC096681.1 GI:15718555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unordered pieces.
Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 144648 bases at least Q40 Consensus quality: 144609 bases at least Q30 Consensus quality: 144809 bases at least Q20 Insert size: 145000; agarcse-fp Insert size: 14517; sum-of-contigs Quality coverage: 10.21x in Q20 bases; agarcse-fp Quality coverage: 10.18x in Q20 bases; sum-of-contis
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Center clone name: 228C
                                                                                                                                                                                                                                                                                            Center: NIH Intramural Sequencing Center Center code: NISC
Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                          Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                   ----- Summary Statistics
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Pred. No. 1
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sum-of-contigs
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NOTE: This is a 'working draft'

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    Center: Washington University Genome Sequencing Center Center code: WUGSC Center code: WUGSC WUGSC Center code: WUGSC And Center code: WUGSC Cente
                                                                                                                                                                                                                                                                              Submitted (28-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                            MO 63108, USA
On Jun 14, 2000 this sequence version replaced gi:7715652
                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 148198)
Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, 9 unordered pieces
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HOMO sapiens chromosome 11 clone RP11-223K12, WORKING DRAFT
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                                                                                                                                                                  ---- Genome Center ----
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clone_end:SP6
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Project Information
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Insert size: 147398; sum-of-contigs
Quality coverage: 4.53 in Q20 bases; agarose-fp
Quality coverage: 4.67 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-primer ET; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2756
12254
12354
12354
123568
22568
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22663
37603
37703
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11054
66694
66694
66794
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115956
                                                                                                                                                                                                                                                                                /note="assembly_name:Contig8" 51154 .66693
                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig7"
37703. .51053
                                                                                                                                                                                                             66794.
                                                                                                                                                                                                                        vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                                    2856. .12253
/note="assembly_name:Contig5"
                                                                                                       116056.
                                                                                                                  vector_side:right"
                                                                                                                                                                                                                                             clone_end:T7
                                                                    /note="assembly_name:Contig12"
34635 c 33776 g 40404 t
                                                                                                                                          clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig6"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .148198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                      /note="assembly_name:Contigl1
                                                                                                                                                                                         /note="assembly_name:Contig10"
                                                                                                                                                                                                                                                               /note="assembly_name:Contig9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RP11-223K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116055: gap of unknown leng
148198: contig of 32143 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115955: contig of 29975 bp in
17.0%;
56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2755: contig of 2755 bp in length 2855: gap of unknown length 12253: contig of 9398 bp in length 12353: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66793: gap of unknown length 85880: contig of 19087 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85980: gap of unknown length
                                                                                                                                                                              .115955
                                                                                                                                                                                                                                                                                                                                                                                           . 22567
                                                                                                                                                                                                                 .85880
                                                                                                         .148198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7: gap of
2: contig
2: gap of
2: gap of
3: contig
3: gap of
3: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of contig
Score 35.8; D
Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown length
of 13351 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 14935 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 10214 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown length
                  DB
                  2;
                                                                        806 others
                    Length 148198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
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AC084337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58974 CTGGGGATGGGGATATGGCAGGTGGGTCAGGGTCCCATGGGTTCACCCTTTCTTGCTCT 59032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castie, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Fitzlugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Spencer, B., Stange-Thomann, N., Stojanovic, N., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGGGGCGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCACAATCCTTCCCAGCCCCAGGGCAGATAGGCAAAGGACTTGCCTACTTCTGTAGGGC 58973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCCCTGCTTTTGGGGGGG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-OCT-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 10, 2002 this sequence version replaced gi:16974143. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 176831)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone CTD-2010I16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC084337 176831 bp DNA linear Homo sapiens chromosome 11 clone CTD-2010I16 map 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC084337.4 GI:18643480
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                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
as soon as it is available and the accession number will be preserved.

1 22120: contig of 22120 bp in length
                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 176831)
                                                                                                                                                                                                                                                                                                                                     Center clone name: 2010_I_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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SEQUENCING
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Job time : 1042.58 secs
              Search completed: November
                                                               Db 101639 CCCACAATCCTTCCCAGCCCCAGGGCAGATAGGCAAAGGACTTGCCTACTTCTGTAGGGC 101698
                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                    BASE COUNT
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                                                                                                                                                                                                              Local Similarity hes 67; Conserv
                                                                                                97 CAGGGGCGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCT 155
                                                                                                                                                                   37 CCCAGAAAGCACAGCTGACTTAGGGAAAGGTCTGGGAAAAATCTCCCTGCTTTTGGGGGGG 96
                                                                                                                                                                                                                                                                                                    46586 a
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         22121 22220: gap of 100 bp
22221 176831: contig of 154611 bp in length
                                                                                                                                                                                                                                                                                                /clone_lib="CITD Human BAC"
42824 c 39611 g 47521 t
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                                                                                                                                                                                                                                                                                                                                                      /map="11"
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56.3%;
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                                                                                                                                                                                                                             Score 35.8; DB 2; Pred. No. 2.4;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                            52; Indels
                                                                                                                                                                                                                                                                                                    289 others
                                                                                                                                                                                                                                              Length 176831;
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Run
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No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
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    pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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    13.8
13.3.3
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12.99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/FCTUS_COMB.seq:*
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US-09-817-180-1
PCT-US96-01735-5
US-08-949-125-49
US-08-949-125-49
US-09-318-448-20
US-09-318-274A-6
US-09-162-274A-6
US-09-162-274A-6
US-09-328-111-83
US-09-328-111-83
US-09-328-111-83
US-09-38-111-10
US-08-367-841A-10
US-08-367-841A-10
US-08-367-841A-43
PCT-US95-07201-43
US-08-814-095-7
US-08-944-838-1
US-08-974-380-1
PCT-US95-14024-2
US-08-977-492-31
US-08-977-492-31
US-08-977-492-31
US-08-977-492-31
US-08-98-616-844-7
US-08-99-654-7
US-08-944-868A-7
US-08-944-868A-7
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                                                                                                                                                                                                                                                                                                    Sequence 4, Appli
patent No. 5185262
Patent No. 5185262
Sequence 6, Appli
Sequence 14, Appl
Sequence 13, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
  Sequence 10, Appl
Sequence 43, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 1, Appli
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Sequence 2, Appli
Sequence 3, Appli
Sequence 31, Appli
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Sequence 7, Appli
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Sequence 83,
Sequence 10,
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STREET: 30 Rockefeller CITY: New York STATE: NY COUNTRY: USA ZIP: 10112-0228 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette

| RESULT 2 PCT-US96-01735-5 ; Sequence 5, Application PC/TUS9601735 ; Sequence 5, Application PC/TUS9601735 ; GENERAL INFORMATION: APPLICANT: Marks, Andrew R. ; TITLE OF INVENTION: HUMAN T CELL INOSITOL 1,4,5,-TRISPHOSPHATE ; TITLE OF INVENTION: RECEPTOR ; UMBER OF SEQUENCES: 8 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond ; STREET: 30 Rockefeller Plaza ; CITY: New York | Query Match Query Match Best Local Similarity 54.1%; Pred: No. 2.2; Matches 59; Conservative 0; Mismatches 50; Indels 0; Gaps 0; Matches 59; Conservative 0; Mismatches 50; Indels 0; Gaps 0; Qy 55 CTTAGGGAAGGTCTGGGAAAATCTCCCTGCTTTTGGGGGGGAGGGGGGGG | RESULT 1 US-09-817-180-1 Sequence 1, Application US/09817180 Sequence 1, Application US/09817180 Patent No. 6340584 GERRAL INFORMATION: APPLICANT: GAN, Weiniu et al. APPLICANT: GAN, Weiniu et al. TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: CL001183 CURRENT APPLICATION NUMBER: US/09/817,180 CURRENT APPLICATION UNMBER: US/09/817,180 CURRENT FILING DATE: 2001-03-27 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 2674 TYPE: DNA ORGANISM: Human US-09-817-180-1 | 2 1067 4 5 PCT-US97-U/289-6 Sequence 1, 2 21067 4 US-09-045-193-1 Sequence 1, 2 2517 1 US-07-906-930E-1 Sequence 1, 2 2939 1 US-07-906-930E-3 Sequence 3, 2 15297 4 US-09-817-180-3 Sequence 3, 2 15297 4 US-08-47-823-1 Sequence 3, 2 1952 3 US-08-947-823-1 Sequence 3, 2 1952 3 US-08-480-784-34 Sequence 3, 2 195-08-480-784-34 Sequence 3, 2 195-08-487-002-34 Sequence 3, 3 195-08-487-002-34 Sequence 3, 3 195-08-488-011B-34 Sequence | 26 12.4 6407 3 US-08-944-496-7 Sequence 26 12.4 8106 4 US-09-135-241-1 Sequence 25.8 12.3 972 1 US-07-940-605A-9 Sequence 25.8 12.3 972 2 US-08-690-096-9 25.8 12.3 2972 2 US-08-690-096-9 25.6 12.3 2972 2 US-08-690-695-1998-8 Sequence 25.6 12.2 548 1 US-09-224-110-6 Sequence 25.6 12.2 548 4 US-09-224-110-6 Sequence |
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SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:

COMPUTER: IBM COR OPERATING SYSTEM:

IBM Compatible

DOS

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US-08-949-155-49/c

Sequence 49, Application US/08949155

Patent No. 6271436

GENERAL INFORMATION:
APPLICANT: Piedrahita, Jorge A
APPLICANT: Bazer, Fuller W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 8791 base pairs
             ZIP: 77210-4433

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   TITLE OF INVENTION: Compositions and methods for the TITLE OF INVENTION: Generation of Transgenic Animal Species NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5551 AGTTATCGACCTCATCATGAAC 5572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5491 GGGTGAGATGAGTCTGGCCGAGGTTCAGTGTCACCTTGACAAGGAGGGGGGCTTCCAATCT 5550
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: ci
HYPOTHETICAL: NO
ANTI-SENSE: NO
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APPLICATION NUMBER: 08/386,039
FILING DATE: 09-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 TGCTCTAGACCGCCTCAGACAC 171
APPLICATION NUMBER: US/08/949,155
                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 AGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAAGGTCTGGGAAAAATCTCCCTGCTTTT 89
                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US96/01735 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: A30042 - 165/30555
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGGGGCCAGGGGCGGGGATGAGCCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGAT 149
                                                                                                                                                                                 Houston
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Pred. No. 5.6;
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US-08-785-310A-4/c

Sequence 4, Application US/08785310A Patent No. 5840532

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US-09-318-448-20
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                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 3228
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/09318448 Patent No. 6210950
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                LENGTH: 3228
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILING DATE: 11-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/
PILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: DATE: DATE:
1689 TGCCTGTGAAAGGGGGGTCCAGGAGCCCCAGGCCCACAAGGAGCCCTGAGGCCTGTTGAGA 1630
                                  149 TTGCTCTAGACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hibler, David W. REGISTRATION NUMBER: 41,071 REFERENCE/DOCKET NUMBER: TAITELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: Concurre CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                     89 TGGGGGGGCAGGGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 GTGAGGACTAGGGAGAATGAGCTTGGCATCCCCTCCCATT
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les 56; Conserv
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STRANDEDNESS: single
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Pred. No. 6
                                                                                                                                                            Score 27.8; DB 4; Length 3228; Pred. No. 6.1;
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                                                                                                                                             Mismatches
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5.1;
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GENERAL INFORMATION:

APPLICANT: McKnight, Steven L.
APPLICANT: Russell, David W.
TITLE OF INVENTION: Neuronal PAS Domain Protein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE:

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5185262-2
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TITLE OF INVENTION: DNA FRAGMENT CONTAINING GENE WHICH ENCODES THE FUNCTION OF STABILIZING PLASMID IN HOST MICROORGANISM NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            ; Patent No. 5185262
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                                                                                                                  5185262-2
                                                                                                                                                  :SEQ ID NO:2
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INFORMATION FOR SEQ ID NO: 4:
                                          Matches
                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: UT TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 4184 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                              APPLICATION NUMBER: US/07/c
FILING DATE: 01-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 385,414
FILING DATE: 26-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 GCTTCTGTCCGGGCACGCAGTACCCCTCTAGCACCCTCGGAGGACCCCCGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 GACTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGCAGCGTGGA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 CTCCCTACGCTTCGGGATGCCTGCGGTGGGGCTCTGGAAGGGCAGCGGGCAATCTTGAAA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 21-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 CTCCCTGCTTTTGGGGGGGCAGGGGGGGGGGGATGAGCCCAGGGCCGAGAAGGAACTCTGAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
  LENGTH: 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: SCIENCE & TECHNOLOGY LAW GROUP
T: 268 BUSH STREET, SUITE 3200
SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 13.2%; Score 27.8; DB 2; Length 4184; Similarity 53.2%; Pred. No. 6.7; 59; Conservative 0; Mismatches 52; Indels 0
                                            60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4184 base pairs
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                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double
                                          12.9%; Score 27; DB 6; Length 176; 52.2%; Pred. No. 8.9; ative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/785,310A
                                                                                                                                                                                                                                                    US/07/473,396
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                                                                                  DB 6; Length 1762;
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                                                      0; Gaps
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APPLICANT: KOHAMA, KEIKO; KOBAYASHI, MIKI; KURUSU, YASUROU;
; YUKAWA, HIDEAKI; FUKUSHIMA, MAKIKO
TITLE OF INVENTION: DNA FRAGMENT CONTAINING GENE WHICH
; ENCODES THE FUNCTION OF STABILIZING PLASMID IN HOST MICROORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5185262-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5185262-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-162-274A-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;SEQ ID NO:1:
                                                                                                                                                          ; NAME/KEY: misc_feature
; LOCATION: (1)...(3740)
; OTHER INFORMATION: n = A,T,C or G
US-09-162-274A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/162,274A
CURRENT FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09162274A patent No. 6316188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liggett, Stephen B.
APPLICANT: Galinsky, Raymond E.
APPLICANT: Weinshilboum, Richard M.
                                                                                  Matches
                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lachman, Herb M.

APPLICANT: Lachman, HISTAMINE-N-METHYLTRANSFERASE VARIANTS

TITLE OF INVENTION: HISTAMINE-N-METHYLTRANSFERASE VARIANTS

FILE REFERENCE: 07039/080001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 385,414
FILING DATE: 26-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 CTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAGGAT 194
                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 CTCGATAGCTATTCCTCGACAGCTCGAGCGCATTACCTCCTTGCTAGCTGATGAT 267
                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 CTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAGGAT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 CACTGCGATGGATTGGGCGGAATCCGCTGAAGAAGCTGGCACGCCATTGGACTTTGAAGT 213
214 CTCGATAGCTATTCCTCGACAGCTCGAGCGCATTACCTCCTTGCTAGCTGATGAT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 CCCTGCTTTTGGGGGGGGGGGGGGGGGGGGATGAGCCCAGGGCCGAGAAGGAACTCTGAAGA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                       24 CTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAAGGTCTGGGAAAAATCTCCCT 83
                                                                     12.8%;
Local Similarity 53.9%;
es 55; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                    Score 26.8; DB 4; Length 3740; Pred. No. 14; 0; Mismatches 47; Indels 0
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84 GCTTTTGGGGGGGCAGGGGGGGGGATGAGCCCAGGGCCGAGA 125

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US-09-328-111-83
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08232463 Patent No. 5670367
                                                     1061 AAGCTCCCTCGACCTGCAGCCAAGCTCGG 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: DORNER, F.

APPLICANT: SCHEIFLINGER, F.

APPLICANT: FALKNER, F. G.

TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
                                                                                                           IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                  149 TTGCTCTAGACCGCCTCAGACACTCTCGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPA
OPERATING SYSTEM: PC-E
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                          89 TGGGGGGGCAGGGGCGGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELLERAX: (/--
TELEFAX: 899149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                        29 AAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCCCTGCTTT 88
                                                                                                                                                                                                                                                      Local Similarity
nes 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alexandria
                                                                                                                                                                                                                                                                                                                                  PTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                                                             7218 base pairs
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                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                       12.7%; Score 26.6; DB 1; Length 7218; 11.4%; Pred. No. 21; ative 74; Mismatches 58; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP 91 114 300.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29,768
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                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (47)...(1489)
US-09-487-445-10
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                                                      Matches 51;
                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-328-111-83
                                                                                                                                                                                                                                     SEQ ID NO 10
LENGTH: 1489
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09487445 Patent No. 6258600
                                                                                                                                                                                                                                                                                                       APPLICANT: Hong Zhang
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISHNSE MODULATION OF CASPASE 8 EXPRESSION
FILE REFERENCE: RTS-0107
                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/487,445
CURRENT FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 83
                                                                                                                                                                                   ORGANISM: Mus musculus FEATURE:
                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FOID, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
CURRENT FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 83, Application US/09328111 Patent No. 6262333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEATURE:

NAME/KEY: misc_feature
LOCATION: (1)...(584)

OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 CGGCGCAGCGTGGAGAGGATTTGT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 CAGGTTCCAGACTGACCCGTCAAAGATCCGCAGCGTTCTCGGGCCACCTTCAGTGAACAC 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 CAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGACCGCCTCAGACACTCT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 GGGGCCAACATGCATTGGCTTTGT 509
5 CTTGTTCTTCTCCTCAGCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 12.6%; Score 26.4; DI Similarity 57.1%; Pred. No. 9.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catino, Theodore J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burgess, Christopher C.
Bushnell, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Astle, Jon H.
                                                  Conservative
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                                                          12.6%; Score 26.4; DB 4; Length 1489; 55.4%; Pred. No. 13;
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                                        Mismatches 41; Indels
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US-08-257-963B-10
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                                                                                                                           US-08-257-963B-10
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SEQUENCE CHARACTERISTICS:
LENGTH: 7210 Bass
                                                            Matches
                                                                                           Query Match
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 6869
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Patricia; Schwartz, Joan P.; APPLICANT: Taniwaki, Takayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1174 CTTCGAGCAACAGAACCACACTTTAGAAGTGG 1205
                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
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                                                                                                                                   IDENTIFICATION METHOD: OTHER INFORMATION: 7.2 kb No. 5840686 1 fragments OTHER INFORMATION: Derived from human placental grants.
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                             22 GCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCC 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                              Local Similarity
                                                                                                                                                                                                      NAME/KEY: JT106
                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                   LIBRARY: DASH II
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                                                             Conservative
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                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                              Unknown
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                                                                            12.5%;
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DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
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Pred. No. 28;
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                                            Matches
                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
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                                                                                                                                                                                              FEATURE:
NAME/KEY: JT6A
                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
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OTHER INFORMATION: 7.
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OTHER INFORMATION: ge
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              22 GCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCC 81
                                                          Local Similarity
                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                            LIBRARY:
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                                            Conservative
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                                                                                                                                                                                                                                                        Human
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                                                                                                                                                                                                                                                                                                                    Double
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DERIVED FACTOR: CHARACTERIZATION
ORGANIZATION AND SEQUENCE OF THE
                                                                                                                 7.0 kb No. 6319687 1-No. 6319687 fragment; Derived from human placental genomic DNA; also referred to as JT106
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Pred. No. 28;
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   Matches
                                 Query Match
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 7210 Base Pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9:
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2:
FILING DATE: 07-JUN-1994
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                           FEATURE:
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                   Local
                                                                                   OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                       IDENTIFICATION METHOD:
TONNORMATION: 7.0 kb Not 1-Not
The Thing Martine T.0 kb Not 1-Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: DOROTHY R. AUTH REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: New York
                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                             TYPE: Nucleic Acid
STRANDEDNESS: Doub
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                                                                                                                                                       NAME/KEY: JT6A
LOCATION:
                                                                                                                                                                                                           LIBRARY:
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                 Similarity
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   Conservative
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                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                 Unknown
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                                                                                                                                                                                                                                                                               Genomic DNA
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                                                                                                                                                                                                                                                                                                                 Double
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                12.5%;
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DERIVED FACTOR: CHARACTERIZATION
ORGANIZATION AND SEQUENCE OF THE
                                                                                   fragment; Derived from human placental genomic DNA; also referred to as JT106
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Score 26.2; D
Pred. No. 28;
0; Mismatches
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                                 DB 5;
 48;
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GENERAL INFORMATION:
APPLICANT: Chader,
APPLICANT: Ignacio
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                                                                                                                                       US-08-367-841A-43
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                                                                   Matches
                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 751-684 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 6861 GGCACTCCAGGGAGCAGAAAAGAGGGGTGCAAGGGAGAGGAAATGCGGAGACAGCAGCCC 6920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/9:
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 30-DEC-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6929 CTGCAATTTGGGCAAAAGGGTGAGTGGATGAGAGAGGGCAGAG 6971
                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6869
                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                             MOLECULE TYPE:
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STREET: 37.
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                                                                                                                                                    OTHER INFORMATION: full length genomic OTHER INFORMATION: sequence for PEDF p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                22 GCCTGTCAAGGAAGTCCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCC 81
                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: Unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/2
FILING DATE: 07-JUN-1994
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                     IDENTIFICATION METHOD:
                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                           NAME/KEY: P1-147
                                                                                                                                                                                                                                                                                                               TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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                                                                                                                                                                                                                                                                                                           Nucleic Acid
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                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chader, Gerald J.; Rodriguez,
Ignacio R.; Mazuruk, Krzysztof;
                                                                                                                                                                                                                                                                             Unknown
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                                                                                                                                                                                                                                                                                               Double
                                                                                   12.5%;
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DERIVED FACTOR: CHARACTERIZATION GENOMIC
ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                                                               6849
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Pred. No. 44;
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                                                                   Mismatches
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Search completed: November 6, 2002, 14:20:31 Job time : 42.9733 secs

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                                                                                                                                                                                Score
   32.8
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
   13736207 seqs, 6748477542 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version Copyright (c) 1993 - 2002
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AQ898422
                                                  CNS01TZC
BE336705
                                                                                          BI256085
AG076601
                                                                      BF172864
                                                                                                                                                               AZ971837
                                                                                                                                                                                                                SUMMARIES
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10897.801 Million cell updates/sec
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Compugen Ltd.
BG855275 1024042C0
BG479234 602526449
AA690752 vu57c08.47
BG775847 602716308
B1256085 602978917
AG076601 Pan trog1.
B1831409 603074508
BF172864 MYE0121 M
AL167169 Tetraodon
BE336705 ba99001.y
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BF128928 603075090
BF759824 PM0-CT064
AQ889422 HS_3135_B
AL108399 Drosophil
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| AG002170 AG002169 BI463395 AA153765 AU175395 | A1804686 A1184928 A1201132 AA779225 AA543126 B1438774 AG002186 AG002186 AG002187 AG002187 | BB776545 A1561790 CNS05M5S AA788598 AW517011 BF001188 BF195077 AA776500 AW439335 A1874207 BW4773156 BW127741 AW169135 BW127990 |
| AG002170 Homo sapi AG002169 Homo sapi BI463395 603204431 AA153765 mr04b03.r AU175395 AU175395 | 94e04.x 28c02.x 64f09.x 39e07.s 36b12.r c26e06. c26e06. omo sap omo sap | 776545 etrabd. etrabd. 58g10. 990c11. 994h12 094f04 111ff0. 111ff0. 111ff0. 111ff0. 111ff0. 111ff0. |

ALIGNMENTS

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SOURCE
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AZ971837/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                 source
                                                                                                                                                       Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0245 row: B column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                689 bp DNA linear GSS 27-APR-200
2M0245B02R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0245B02 R, DNA sequence.
AZ971837
                                                                                                                                                                                                                                                                                                                   University of Utah (
University of Utah
Rm. 308, Biomedical
                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 689)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                  High quality sequence stop: 689
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                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
                                                                                                                                                                                                                                                                                                     USA
                                     /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                    /clone="UUGC2M0245B02"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                             Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCTTGCTTTTTCTTCTGGGCTTGCTGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGG 78
                                                                                                                                                                                                                                                                                                                       Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
                                                                                                                    Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 772)
1 (bases 1 to 772)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRI human cDNA project
                                                                                                                                                                                                                                                                                                               81-438-52-3952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 772 bp mRNA linear 1
           /organism="Homo sapiens"
                                                                                  Location/Qualifiers
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/note="Vector: PWD42nv; Purified genomic DNA from M.
/nusculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
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68.5%;
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Pred. No. 0.00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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L 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 GACCGCCTCAGACACTCTCGGCGCAGCGTGGAGAGGATTTGTGCA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 TAAATCTGGAGGAGGAAGCTCTTGCCTGGGGGAACATTACAGAGCCTGGAGCATAGGTTA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 CCCAAGAAGCACAGGACCACCTGGGAAAGACAGGGGACAGTCTCCCAGCCTGGGCACCCT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P., McDermott,J.P., Sliflow,C., Stern,D. and Surzycki,R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2
Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pospoz/b 939 bp mRNA linear EST 29-MAY-;
1024042C07.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
BG855275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duke University
Durham, NC 27708-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG855275.1 GI:14236459
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           199
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919 613 8177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chauser@duke.edu
           þ
žAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."

336 c 140 g 264 t
                                                                                                                                          XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. Polya mRNA was purified from each sample, pooled and CD0. Solve and CDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. PBluescript II SK-plasmids were excised from the lambda can be supplessed to the lambda can b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/note="vector: pwB188FL3
/note="vector: pwB18FL3
170 t 3 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/clone="HEMBA1005931"
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52.1%;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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GAGAAGG 128

17 GATTCGG 11

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Matches Query Match

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Conservative

Local

Similarity

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Homo sapiens

human AU119486.1 AU119486/c

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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 GAAGGTTCACAGAACGTGGCGAGTGGGGAAGAACAGGTAACGCGGTTATGGGGAAGCGAGG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        516 GGGGGGGGGGGGGAGGGAACGGGAATGAAGGCAGAGGAAACGGGTGAAAAGGATAGA 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 GARAGCACAGCTGACTTAGGGARAGGTCTGGGARAAATCTCCCTGCTTTTTGGGGGGGGCAGG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 16.6%;
Local Similarity 55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                        114 CCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGACCGCCTCAGACACTC 173
                                                                                 427 AATTGGCAAAGCTGTGGAAGACTCCACAGCCCTACTGGGAGGCACGGAGGGGTGGCGAGG 486
487 CCAGGCTCAGCTGGAAGCTCAGAAAGCCCACGCAGGACTTCCAGAGGGCCACAGAGGTGC 546
                                                                                                                          Local Similarity
es 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
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602526449F1 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:4649772 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG479234.1 GI:13411513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1430 row: b column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 771)
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                                                                                                                                                                                                                                                                              /CLONE-ILM-WGC_21"
/Clone_Ilb="NHH_WGC_21"
/tissue_type="choriocarcinoma"
/tissue_type="choriocarcinoma"
/lab_host="by10B (phage-resistant)"
/lab_host="by10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_1 Size_selected >500bp
Site_2: ECORI; CDNA made by oligo-dT priming;
placentionally cloned into ECORI/XhoI sites using the
placetionally cloned into ECORI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected by
for average insert size 1.8kb. Library constructed by
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
of California, Berkeley) using ZAP-CDNA synthesis kit
of California and Superscript II RT (Life Technologies)."
(Strategene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:4649772"
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                                                                                                                                                                                                 16.3%;
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                                                                                                                                                                              0;
                                                                                                                                                                                                 Score 34.2; DB 10; Length 771; pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                771 bp
                                                                                                                                                                                 Mismatches 68;
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                                                 105 GGGGATGAGCCAGGGCCGAGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGA 158
                                                                                                      Match 16.2%;
Local Similarity 56.1%;
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AA690752
AA690752
Vu57c08.rl Soares_mammary_gland_NbMMG Mus musculius cDNA clone
Vu67c08.rl Soares_mammary_gland_NbMMG Mus musculius cDNA clone
Vu67c08.rl Soares_mammary_gland_NbMMG Mus musculius cDNA clone
Vu67c08.rl Soares_mammary_gland_NbMMG Musculius cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA690752.1 GI:2691688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            possible reversed clone: similarity on wrong strand Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;, mRNA sequence.
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima normalor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              7 3']; double-stranded cDNA was ligated to Eco RI addaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares_mammary_gland_NbMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:1195502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                    Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco) with a trand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
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                                                                                                                                                                                                                                                                                                                155 c
                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                      162 g
                                                                                                                                                                                                    Score 34; DB 9; Length 623; pred. No. 24;
                                                                                                                                                                                  Mismatches 50; Indels
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SOURCE
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                                                                                                                                                                                                                                                                     828 GGAACTGGGCGCATGGAGGCGGCGCCACGGAGGGCCAAAGCGGACNCCG 877
                                                                                                                                                                                                                                                                                                                                                768 GTGCCTGGAACCACAGCTGGCCTGGACCAGGACAGTGAAGCAATAACCTGGAGCTAGGGC 827
                                                                                                                                                                                                                                                                                                            95 GGCAGGGGGGGGGTGAGGCCAGGGCCGAGAAGGAACTCTGAAGACTCCG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                     35 GTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCTCCCTGCTTTTGGGGG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                   BI256085 695 bp mRNA linear EST 20-JUL-2001 602978917F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5123621 5',
                                                           house mouse
                                                                                 BI256085.1 GI:14810144
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://image.llnl.gov
Plate: LLCM1707 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 895)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by Oligo-dT priming: XhoI;
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit Note: this is a NIH_MGC Library." (Life Technologies).

Note: this is a NIH_MGC Library." 1 others
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/clone_lib="NIH_MGC_48"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 TCTGGACTGGAGCCCTGCTCGGGCACGGCAGCAGCAGCAGCTCCGAGCAGCTCTGAGGG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 CTCCGTAG 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 CAGGCTGTGAGAAAGCTGCCGCAACCACAGTTCCGGGATGCAGGCCCTGGTGCTACTCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 CAGCCTGTCAAGGAAGTCCCAGAAAGCACAGCTGACTTAGGGAAGGTCTGGGAAAAATCT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                                       rullyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                       Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                               Fujiyama,A.,
                                                                                                                             Unpublished
                                                                                                                                                   BAC end
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
                                                                                                                                                                                                                                                                       GSS; GSS (genome survey sequence).

Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-070N17.F.
                                                                                                                                                                                                                                                                     Pan troglodytes
                                                                                                                                                                                                                                                                                                                                     AG076601.1 GI:16628403
GSS; GSS (genome survey
                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes DNA, clone: PTB-070N17.F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAMI1302 row: b column: 06
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Similarity 53.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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                                                                                                                                     sequences of Library PTB
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/clone="IMAGE:5123521"
/clone=lib="NGI_CGAP_LI9"
/clone_lib="NGI_CGAP_LI9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Priner: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 223 c 187 g 137 t
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/strain="FVB/N"
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Pred. No. 33;
0; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 ACACTCTCGGCGCAGCGTGGAGAGGATTTGTG 199
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                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                Plate: LLAM11413 row: p column:
                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 258)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                               High quality sequence stop: 258.
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603074508F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5166577 5',
                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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R.Site 2 : SacI.
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              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5166577"
                                                                            Location/Qualifiers
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/clone_lib="PTB Chimpanzee Male BAC Library"
178 c 237 g 261 t 15 others
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/sex="male"
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51.3%;
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Pred. No. 35;
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Best Local Similarity 67.1%;
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                                                                                                                                                                                                                                                                                                                                                                                      FORWARD: 5'-GCCAAGCTCGAAATTAACCCTCACTAAAGGG-3'
BACKWARD: 5'-CCAGTGAATTGTAATACGACTCACTATAGGGCG-3'
Seq primer: 5'-GAAATTAACCCTCACTAAAGG-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University Health Network
610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada
Tel: (416) 946-4639
Fax: (416) 946-6546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The transcriptional phenotype of myeloma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: A. Keith Stewart, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claudio, J.O., Tang, H., Khan, E.M., Voralia, M., Li, Z., Cukerman, E., Franciso-Pabalan, O., Liew, C.C. and Stewart, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claudio, J.O.,
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BF172864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     k.stewart@utoronto.ca
/note="Vector: Lambda Zap Express; Site_1: EcoRI; Site_2: XNOI; Myeloma cells from multiple myeloma pattents' bone marrow were purified by magnetic cell sorting. mRNA were purified and an oligo d(T)18 primer containing XhOI restriction site was used to prime first strand synthesis using M-MLV reverse transcriptase. To protect the cDNAs from XhOI digestion in subsequent cloning step, the nucleotide analogue 5-methyl-dCTP was added to the
                                                                                                                                                                                  /tissue_type="Blood"
/cell_type="myeloma"
/cv_stage="multiple_myeloma"
                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone_lib="Myeloma (MYE) cDNA library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NHIMGC Library."
                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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/lab_host="DH108"
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acthopterygil; Neopterygil; Teleostel; Euteleostel; Neoteleostel; Acanthomorpha; Acanthopterygil; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS; genome survey sequence 
Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 195P21 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                         Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
                                                                                                                                                                                                                                                                                                                                                                                     Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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2 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   freshwater pufferfish Tetraodon nigroviridis
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       139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotide mixture and [a-32P]dATP was added to monitor the quantity and quality of first strand synthesis. After second-strand synthesis and blunting of cDNA termini, ECORI adapters were ligated, followed by kinase treatment and digestion with XhoI. The cDNAs were then size-fractionated using Sephacryl S-500 column and then size-fractionated using Sephacryl S-500 column and then ligated into ECORI and XhoI digested Lambda Zap Express vector. The ligation product was packaged using Gigapack II packaging extract. The library had primary titre of approx. 1x106. Clones from the primary library were randomly selected for single pass sequencing."
                             PUC-Ori"
                                                                                                    /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="195P21"
                                                    /clone_lib="G"
/note="Genoscope sequence ID : COAG195CH11SP1~end
                                                                                                                                                                                                      Location/Qualifiers
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Pred. No. 33
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1 (bases 1 to 597)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Other_ESTs: ba99d01.x1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Clone="IMAGE: 270007"
/Clone_Tib="NIH_MGC_14"
/clone_type="renal cell adenocarcinoma"
/tissue_type="renal cell adenocarcinoma"
/tissue_type="renal cell adenocarcinoma"
/tissue_type="renal cell adenocarcinoma"
/lab_host="hll0B (phage=resistant)"
/note="lenal (phage=resistant)"
/note="l
                                                                                                                                                                                                                                                                                                                                                                                                                                              adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University Of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 210 c 152 g 106 t
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/clone="IMAGE:2958049"
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Pred. No. 39;

 Mismatches

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Pred. No. 4
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RESULT 14
BG035198/c
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                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                           GCCGGGAAGG 544
                                                                                                                            602324706F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4413048
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                             Homo sapiens
                                                                                                        BG035198
                                                                                                                      mRNA sequence.
                                                                                   BG035198.1 GI:12429091
                                                                                                                                                                BG035198
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  this is a NIH_MGC Library."
1 227 c 203 g 121 t
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/lab_host="DH10B"
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/clone_lib="NIH_MGC_119"
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67.1%;
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Pred. No. 4
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COMMENT
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Best Local Similarity
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TITLE
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                                                          Laboratory of Cancer Genetics Ludwig Institute for Cancer Research
                                                                                                        Contact: Simpson A.J.G
                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                               l (bases 1 to 386)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                         Brazi.
                                                                                                                                                                            sequence tags
                                                                                                                                                                                                                    Simpson, A.J
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAMI0138 row: k column: 01
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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+55-11-2704922
                                                                                                                                              Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/tissue_type="adenocarcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MCC_Library."
a 308 c 215 g 162 t
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Pred. No. 46;
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FEATURES
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Search completed: November 6, 2002, 16:07:08 Job time: 269.086 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.7%; Score 33; DB 10; Length 386; Best Local Similarity 53.5%; Pred. No. 40; Matches 69; Conservative 0; Mismatches 60; Indels
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                                                                                                                                                                                                                         253 CCAAGCCAAGCCAAATGGCCCCATCATCTCTCGCAAGAGCAGGAGAATACCTGGGGGCAG 312
                                                                                                                                                                                                                                                                              123 AGAAGGAACTCTGAAGACTCCGTAGATTGCTCTAGACCGCCTCAGACACTCTCGGCGCAG 182
                                                                                                                                                                                                                                                                                                                                   313 AGGCCATAG 321
                                                                                                                                                                       183 CGTGGAGAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-CT0642-
151200-001-g01&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 22
High quality sequence start: 109.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Togan: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from OSETES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions. 81 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0642"
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: ./cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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1660
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Listing first 45 summaries
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                                                                         DB
                   US-08-142-439A-1
US-09-08-869-477-1
US-09-09-119-1
US-09-09-119-1
US-09-371-507-1
US-08-32-177A-8
US-08-22-177A-8
US-08-545-196B-14
US-08-545-196B-14
US-08-545-196B-14
US-08-72-177A-14
US-08-72-177A-10
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| US-09-018-864A-1 US-08-871-267B-1 US-09-618-419-1 | US-08-452-655B-3 US-08-450-582-3 US-08-871-266B-1 US-08-819-458A-1 | US-07-741-940-3 US-08-289-548A-3 US-08-452-654-3 | US-09-280-799-133 US-08-793-044-1 US-08-532-814-1 US-09-225-509-1 | US-08-702-525-3 PCT-US95-02576-3 US-09-031-962D-5 US-09-078-294-3 |
| Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli | Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli | Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli | 1,1,133 | Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 3, Appli |

ALIGNMENTS

RESULT 1 US-08-142-439A-1

Sequence 1, Application US/08142439A Patent No. 5670360 GENERAL INFORMATION:

APPLICANT: Thorens, TITLE OF INVENTION:

Receptor for the Glucagon-Like-Peptide-1 (GLP-1)

NUMBER OF SEQUENCES: 9

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APPLICATION NUMBER: US/08/142,439A
FILING DATE: 24 NOV-93
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 398/92
FILING DATE: 25 MAR-92
PRIOR APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23 MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3756.204-US
TELECHONE: 212 867 0123
TELEPHONE: 212 867 0123
                                                                                                                                                                                                                    TELEFAX: 212 867 0298 INFORMATION FOR SEQ ID NO:
                                                                        TOPOLOGY: linear MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                        HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 3066 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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STATE: New York
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                                     ORGANISM:
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NAME/KEY: CDS
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; LOCATION:
US-08-869-477-1
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US-08-142-439A-1
 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                      ORIGINAL
                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 212 867 0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                               MOLECULE TYPE:
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                                                                                                                                 HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 TCTTCC 290
                                                                                                                                                                                                                                                                                                          NAME: Harrington, James J
REGISTRATION NUMBER: 38,7
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-NOV-93
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-MAR-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                      ORGANISM:
                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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Local Similarity 92.4%;
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                                                                                                                     SOURCE:
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Y: U.S.A.
                                                                                                                                                                                                       3066 base pairs
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                                                                                                                                                               linear
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5 Lexington Avenue, Suite 6400
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 3.5%;
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                                                                                                                                                                                                                                                                                                      38,711
38,711
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 Score 58;
Pred. No.
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Pred. No. 4e-08;
DB 2;
4e-08;
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               Length 3066;
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; ORGANISM: Chlamydomonas reinhardtii US-09-371-507-1
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                                                                                                                                               SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
     Matches
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09371507 Patent No. 6346656
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Patent No. 6160206
                       Best
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APPLICANT: BOYNTON, John E.
APPLICANT: GILLHAM, Nicholas W.
APPLICANT: HARRIS, Elizabeth H.
APPLICANT: HARRIS, Porphyrin Accumulating-Type Herbicide Resistance Gene
FILE OF INVENTION: Porphyrin Accumulating-Type Herbicide Resistance Gene
FILE REFERENCE: Substitute sequence listing
CURRENT APPLICATION NUMBER: US/99/371,507
CURRENT FILING DATE: 1999-08-18
CURRENT FILING DATE: 1999-08-18
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APPLICANT: BOYNTON, John E.
APPLICANT: GILLAM, Nicholas W.
APPLICANT: HARRIS, Elizabeth H.
TITLE OF INVENTION: Porphyrin Accumulating-Type Herbicide Resistance Gene
FILE REFERENCE: substitute sequence listing
CURRENT APPLICATION NUMBER: US/09/009,119
CURRENT FILING DATE: 1998-01-20
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/009,119 PRIOR FILING DATE: 1998-01-20
                                                                                                            TYPE: DNA
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                                                                                                                          LENGTH: 3381
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Local Similarity 81.7%;
   1 Similarity 67; Conserv
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   Conservative
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                  3.5%;
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 Score 58; DB 4; Le
Pred. No. 4.2e-08;
0; Mismatches 15;
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Pred. No. 4.2e-08;
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              RESULT 6
US-08-772-440-33
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Sequence 33, Application US/08772440
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Best Local :
                                                                                                                                                                                                                     Matches
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TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Gillham, Nicholas W.
APPLICANT: Harris, Elizabeth H.
TITLE OF INVENTION: Porphyrin-Accumulating Type Herbicide
TITLE OF INVENTION: Resistance Gene
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1712 GTCCTGCAGCCCCGAACCCCGC 1691
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NAME: MUTPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 2185-110P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 3383 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                287 TTCCCTCCCTCCACTTCCTCCC 308
                                                                                 1713 GTCCTGCAGCCCCGAACCCCGC 1692
                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                 287 TTCCCTCCCTCCACTTCCTCCC 308
                                                                                                                                                                                 TELEPHONE: (703) 205-8050
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Falls Church
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/09098
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8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                     Conservative
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 Mismatches

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Patent No. 6046158
GENERAL INFORMATION:
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APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DE
TITLE OF INVENTION: LECTINS,
TITLE OF INVENTION: THEREOF
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NAME/KEY: modified_base
FOCATION: 3497..3607
mod
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NAME/KEY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: modified_base LOCATION: 3406..6470 OTHER INFORMATION: /mod_OTHER INFORMATION: /note
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LOCATION:
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            LOCATION: 3457..9998
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "W = A OI T"
                                                                                                OTHER INFORMATION: /note=
                                                                                                                    OTHER INFORMATION:
                                                                                                                                  NAME/KEY: modified_base LOCATION: 3405..6871
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/note= "R = A or
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/note= "N = A or C or G
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US-08-222-177A-8/c
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                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILLNG DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (668) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08222177A Patent No. 5582979
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                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Weber,
                                 TISSUE TYPE: B
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
POSITION IN GENOME:
                                                                                                   MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2825 GAGNNNNAAATTCAATANATAAAATTCTCTTTTGGCAGNTGAGTTCCTC 2872
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                    CLONE:
                                                                  INDIVIDUAL ISOLATE
                                                                                         ORGANISM:
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8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                              (808)
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                                                                                    Homo sapiens
                                                                                                                                       linear
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3595..9999
                                                   Blood
                                                                                                                     DNA (genomic)
                                                                                                                                                        double
                                                                                                                                                                                                                                                             831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.5%;
56.0%;
                                                                  Caucasian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58; DB 3; Length 10409; Pred. No. 8.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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US-08-920-422-17

: Sequence 17, Application US/08920422A

: Patent No. 6255473
                                                                                                                                                                                                                              RESULT 8
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      GENERAL INFORMATION:

APPLICANT: Vitek, Michael P.

APPLICANT: Mitsuda, No. 6255473iaki

APPLICANTION: Presenilin-1 Gene Promoter

FILE REFERENCE: VITEKPRESENILIN

CURRENT APPLICATION NUMBER: US.08/920,422A
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
CURRENT FILING DATE: 1997-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /standard_name= "Only or PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          122 ACACACACACACACACTCTCTCTCTCTCTCTG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                        283 TTTCTTCCCTCCCTCCACTTCCTCCATTCTCTGTG 318
                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: Weber, James L.
AUTHORS: May, Paula E.
TITLE: Abundant Class of Human DNA Polymorphisms
TITLE: Which Can Be Typed Using the Polymerase Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGES: 388-396
DATE: 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Weber, J. L. AUTHORS: May, P. E. TITLE: Dinucleotide repeat polymorphism at the D2S71 TITLE: locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: complement (180..199)
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "PCR primer"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 1..200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: complement (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /rpt_type= "tandem"
OTHER INFORMATION: /rpt_family= "(dC-dA)n.(dG-dT)n"
OTHER INFORMATION: /citation= ([2])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 53..72
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2203-
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region 105..178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence= EXPERIMENTAL
/standard_name= "PCR primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /standard_name= "Only one strand sequenced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /citation= ([1])
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 200;
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US-08-750-064-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08750064
Patent No. 6040142
GENERAL INFORMATION:
APPLICANT: MELKI, JUDITH
APPLICANT: MUNICH, ARNOLD
TITLE OF INVENTION: METHOD AND PROBES FOR DETECTING MARKERS
TITLE OF INVENTION: BOUND TO THE LOCUS OF CHILD SPINAL MUSCULAR ATROPHIES
                                        Query Match
            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 67; Conservative
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                                                                                                                                                                                                                                                         TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35891 ACACACACACACACACAAACA 35913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 22
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                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,064
FILING DATE: 29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                         ANTI-SENSE:
                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENCTH: 372 base pairs
TYPE: nucleotide
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA;
APPLICATION UNMBER: FR 94/06856
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                         NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 960-26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 48974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 ACACACACACACACACACACA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 75.5 nes 71; Conservative
                                                                                                                                                                          TOPOLOGY:
                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 NOI
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22201-4714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                           (703) 816-4000
                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                          double
                     3.4%; Score 57.2; DB 3; Length 372; 75.5%; Pred. No. 1.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5%; Score 57.4; DB 4; Length 48974; 80.7%; Pred. No. 3.8e-07;
                                                                                                                                                                                                                                                         1:
     0; Mismatches
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   1.8e-08;
ches 23;
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   Indels
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Gaps
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; Sequence 4, Application US/09078294
; Patent No. 6265211
                                ; GENERAL INFORMATION:
                                                                                 US-09-078-294-4
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                                                                                              RESULT 11
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                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08545196B Patent No. 6080577
           APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 205-80 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION UNMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "SYNTHETIC DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MELKI, JUDITH
APPLICANT: MUNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                          145 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 178
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                        284 TICTICCCTCCCTCCACTTCCTCCCATTCTCTGT 317
                                                                                                                                                                                                    145 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 178
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 TTCTTCCCTCCCTCCACTTCCTCCATTCTCTGT 317
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                                                                                                                                                                                                                                                                                      Match 3.4%;
Local Similarity 75.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71;
                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                 372 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: BIRCH, STEWART, KOLASCH AND BIRCH, LLP PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                 Score 57.2; DB 3; Length 372; Pred. No. 1.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2121-110P
                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                       23;
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                                                                                                                                                                                                                                                                     0;
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RESULT 12
US-08-222-177A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08222177A Patent No. 5582979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTMARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Weber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Nucleotide sequence of NC-contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52119 ACACACACACACACACCCCTATTCATTGCCAACAGTAATAGAGTTGCTTCTTTACT 52176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 80246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 223 base pairs
                                                 MOLECULE TYPE: I
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les 80; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                       TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
               ORGANISM: Homo sapiens INDIVIDUAL ISOLATE: Car
                                                                                         TOPOLOGY:
                                                                                                         STRANDEDNESS:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCCTCCCTCCACTTCCTCCCATTCTCTGTGGTCCCAAAGAGATGACCATATTGACT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53717-1914
                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weber, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                         linear
                                                                     DNA (genomic)
                                                                                                         double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/222,177A
                 Caucasian
                                                                                                                                                                                       14:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
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                                                                        ; Sequence 1, Application US/08720484A; Patent No. 5990281
                                                                                                         RESULT 13
US-08-720-484A-1
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                               Query Match
                                            GENERAL INFORMATION:
APPLICANT: DeSauva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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NAME/KEY: misc_feature
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             APPLICANT: Rosenthal, Arnon APPLICANT: Stone, Donna
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAGES: 1990
                                                                                                                                                                        181 ACACATTCTTGCC 193
                                                                                                                                                                                                                                  JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                      279 ATGTTTTCTTCCC 291
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
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LOCATION: complement (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS: May, P. E. TITLE: Dinucleotide repeat polymorphism at the TITLE: D18534 locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: complement (185..204)
IDENTIFICATION METHOD: experimental
                                                                                                                                                                                                                                                                                                                                                                               PAGES: 388-
DATE: 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VOLUME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE:
                                                                                                                                                                                                                                                                                                                 Match 3.4%;
Local Similarity 86.3%;
                                                                                                                                                                                                                                                                                                   63;
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May, Paula E.

Abundant Class of Human DNA Polymorphisms
Which Can Be Typed Using the Polymerase Chain
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                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                         DeSauvage, Frederic
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/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence= EXPERIMENTAL
/standard_name= "PCR primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "PCR primer"
/citation= ([1])
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 Vertebrate Smoothened Proteins
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                                                                                                                                                                                                                                                                                                   Score 57; DB 1; Length 223; 
pred. No. 1.5e-08; 
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                        0,
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NUMBER OF SEQUENCES: 5

ADDRESSEE:

CITY: South San Francisco

1 DNA Way

Genentech, Inc.

California

STATE:

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RESULT 14
US-08-953-823A-1
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08953823A Patent No. 6136958
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                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3854 base pairs
                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,823A
FILING DATE: 30-Sep-1997
                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: VENUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3490 CACCCTCTTACTTC 3503
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WilPatin (Genentech)

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE, DOCKET NUMBER: P10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Svoboda, Craig G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 CACATGTTTTCTTC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1 DNA Way
CITY: South San Francisco
APPLICATION NUMBER: 60/027070
                                 CLASSIFICATION:
                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y Match 3.4%; Score 56.4; DB 2; Length 3854; Local Similarity 85.1%; Pred. No. 1.5e-07;
                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Nucleic Acid
STRANDEDNESS: Sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 30-Sep CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Conservative
                                                                                                                                                                                       94080
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                                                                                                                                                                                                                     California
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Rosenthal, Arnon
Stone, Donna
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                                                                                                                                                                                                                                                               Genentech, Inc
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N: 530
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                                                                                                                                                                                                                                                                                                                   Vertebrate Smoothened Proteins
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RESULT 15
US-08-232-463-14/c
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US-08-953-823A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08232463 Patent No. 5670367
                             INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTLING DATE: 30-Sep-1996
ATTOREY/AGENT INFORMATION:
NAME: SVONDORA, CTAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225_1489
                                                                                                                 NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                           FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                      TELLETAX: (/-
TELEFAX: 899149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3490 CACCCTCTTACTTC 3503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3854 base pairs
TYPE: Nucleic Acid
                                                                                       TELEPHONE: (/U3/C-109)683-4109
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TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                              APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/232,463 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                  nucleic acid
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1800 Diagonal Road,
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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
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Search completed: November 6, 2002, 14:19:56 Job time: 417.027 secs
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                                                                                                                                                                                                                                                                                                              445 TTTTAGGGATTTTTATCTAGCGGCACTCACCTGCTTCCCTGTGAATGTTCAGAATTCACT 504
                                                                                                           625 GCTACTCTAACATTTTGTCTCTCACCTTCCACTTGGTTCTTCAATGGAAAGACTGGATAG 684
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AAI90376 AAK81626 AAC91904

Human Human

polynucleoti immune/haema

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Result
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Listing first 45 summaries
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is derived by analysis of the total score distribution.

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                  immune syste immune/haema
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Human

immune/haema

იიი 000000 c c 0 0 0 0 0 0 0 0 0 misc_RNA 5' flanking region; 5' UTR; untranslated region; murine; glucagon-like peptide-2; GLP-2; receptor; regulator; intestinal epithelium; lateral hypothalamus; promoter; ds. 25-OCT-2001. misc_RNA WO200179290-A2 Key Mus musculus. 5' flanking and 5' UTR of GLP-2 receptor gene. 30-JAN-2002 (first entry) AAH43758; AAH43758 standard; DNA; ധതത 9999 /note= "Punitive transcriptional start site" 1761..1763 /note= "Corresponds to translational start in rat/human GLP-2R gene" 1875..1877 Location/Qualifiers 1656 /*tag= c /note= "Putative translational start site" 168575 143068 143068 143068 143068 143068 149412 152740 415 4858 4858 4858 14858 156153 156153 156153 156271 160271 405 437 574 574 2170 AAI88261 ABA59754 ABA28258 AAF21280 AAA35150 AAA35160 AAA35160 AAA35160 AAA36282 AAA685750 AAF85750 AAF85750 AAF85750 AAF85750 AAF85750 AAF23764 AAF85116 AAF85151 AAS16874 AAA39622 AAK66814 AAI82412 AAS46793 ALIGNMENTS Human chromosome 1
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Human chromosome 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the 5' flanking and 5' UTR of the murine glucagon-like peptide-2 (GLP-2) receptor gene. This sequence may be used in the DNA construct of the invention, such that it is linked for expression with a heterologous gene of interest. This construct
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                                                                          CTTGCCACGTGTGGGTTTTAAGGTTTTTAGGGATTTTTATCTAGCGGCACTCACCTGCTT
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                                                                                                                                                                                                                                                                                                                                                                                           CAATTGAAAGGCACCAACCTCCGTGCTTCCTACCCGTTGTTTTGTTACCGTGTAAACGCA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTCAGGTGGCCAGAGCATCACTGTGTTCAGAACACAACGGCCCACTCAGAACACGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAACCATAAACTGAAGTGGGGTGTTGGTTAGTAAGTAGCCATGAATACCATAAAAATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTACCTTGGAGGATACTGATGGGTTCAAGTGAACTAGGGCAGAGGGTGGAAGGTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGTACCTTGGAGGATACTGATGGGTTCAAGTGAACTAGGGCAGAGGGTGGAAGGTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAACAAACACCCTGGCCTCTTTGAACCCCCACTATTTCTCAGCCCTCAGATGAAGAAGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTGGTCACGTGACTCGGCTGGAAGSCCTGGCTTTGTCTTTTTGCTTGCTGCAGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTGGTCACGTGACTCGGCTGGAAGSCCTGGCTTTGTCTTTTTGCTTGCTGTGCAGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAYCATGAGCTTYCTTTGAGACCCCTAGTGCTAACAGGAATAGTTCCTAACCAGGTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTGTGTGGGGGGGGGGGCAGCAAGCAGAGCCTTAGAGACAGAGAAGAGCCTGCTAG
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                                                                                 TGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGGTAGGTCTGGGAAAAATCTCCCCAAGA 1560
                                                                                                                                                                   AGAAGCCTACCTGGCATGGGGGCCCATCCTCCAGCCATCCGAATCTCAATCTGGTCGT
                                                                                                                                                                                                                         TGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGGGGGTAGGTCTGGGAAAAATCTCCCAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       avian nephroblastoma; avian myeloblastoma virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human nov gene promoter sequence XXXIII fragment 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ36051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ36051 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention includes nucleotide sequences which can hybridise to all or part of the chicken nov gene under stringent conditions (i.e. 50% formamide, 5 x SCC). The promoter sequence from the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequences hybridising to regions of chicken useful as probes for detecting complementary sequences evaluate development and/or differentiation of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9300430-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-1993
                                                                                                                                                                                                                                                                                                                                  The human nov promoter contains several consensus sequences for different transcription factors such as NF1, AP1 and Sp1. It also comprises a sequence of 20 repeats of the TG motif (a possible polymorphic marker). See also AAQ36050 and AAQ36052.
                                                                                                                                                                                                                                                                                                                                                                                                  (i.e. 50% formamide, 5 x SCC). The promoter sequence from the human nov gene, localised to a 2.2kb PstI-HindII fragment and comprising the 283bp upstream of the start of including the start of sequence xxxIII disclosed. The promoter sequence corresponds to sequence xxxIII which is given as three separate fragments in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JAN-1993
                                                                                                                                                                            1025 CAGGGGAAGGGAATCTAGAAAAAAATCGATATGTCAGGAGGTGGGGGAATGCTATTGG 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 45-46; 67pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martinerie C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JUN-1992;
                                                                                                                                                                                                                                                                                                        Sequence 1199 BP; 269 A; 292 C; 248 G; 390 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CNRS ) CENT NAT RECH SCI.
                259
                                                905
                                                                                                            965 CCANATGGCAAAATTCTTTTGACTCTAATCCTTCTAGCTTCACTCAGTCTTAAACCCCCAA 906
                                                                                                                                            139 ATATTTGTACAAAACAGGTGCTTTCTCCCCCCACCATGCGACCCGGGAGCTCCACTGATAT 198
                                                                                                                                                                                                                                 3.9%;
Local Similarity 57.8%;
nes 115; Conserva+***
                                                                                                                                                                                                        79 CAGGGGGAAGAAAATCAGGAAAAAAAAAATTTTAGAAGCATTTCAAGAAGCAAGATGGA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
ACACACACACACACACACA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1993-036377/04.
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perbal B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91FR-0007807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-FR00589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA; 1199
                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                        Score 64.6; DB 14; Length 1199;
Pred. No. 2.6e-08;
0; Mismatches 84; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nov gene
                                                                                                                                                                                                                                          0;
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AAV30918
ID AAV
                                                           RESULT 4
AAF98397
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DXXXX
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                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                      This polynucleotide comprises the 3' portion of a cDNA clone, designated AS63_29 (see also AAV30917), that codes for a novel human secreted protein (see AAW58381). AS63_29 was isolated from a human foetal brain cDNA library using methods selective for cDNAs that encode secreted proteins. The clone is deposited in composite clone ATCC 98232; an oligonucleotide (see AAT99723) is designed to isolate the clone from the composite. Novel cDNA clones (see AAV30916-32) coding for human secreted proteins (see AAW58580-90) are claimed. These can be used for recombinant production of the secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding secreted protein from human cells - useful, e.g. as immunomodulator, antitumour agent, promoters of tissue growth, haemostatic and thrombolytic agents etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agostino MJ, Jacca
TA, Spaulding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV30918 standard; DNA; 245 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-OCT-1997;
25-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein AS63_29 cDNA 3' region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV30918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AS63_29; secreted protein; protein factor; human;
                                                                                                                                                                                                                                                                       Sequence 245 BP;
                                                                                                                                                                                                                                                                                                            proteins for analysis, characterisation, diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Page 69; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-261426/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         845 ACACACACACATAAAGAAA 827
                                                  AAF98397 standard; cDNA; 245 BP
                                                                                                                133 CTTGCTTCCNTCCCCCAGTGCGTTCTGTGATCGCCAAG 170
                                                                                                                                         290
                                                                                                                                                                                           73
                                                                                                                                                                                                                                 Local
                                                                                                                                                                   CCTCCCTCCACTTCCTCCCATTCTCTGTGGTCCCAAAG 327
                                                                                                                                                                                                                                 3.8%;
Similarity 77.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacobs K,
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0740274.
96US-0740274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US19590
                                                                                                                                                                                                                                                                       85 A; 69 C; 38 G; 45 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treacy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lavallie ER,

 Mismatches

                                                                                                                                                                                                                                 Score 63.4; DB 19;
Pred. No. 2.4e-08;
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                                                                                                                                                                                                                                                  245;
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07-JUN-2001

(first entry)

AAF98397;

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RESULT 5
AAI8828/c
ID AAI888
XX AAI888
XX AAI888
XX HAMBA
AC AAI888
XX HAMBA
AX HAMBA
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                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              proteins AAB90667 - AAB90750. The CDNA clones are isolated from various tissue types, and may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression. The polypeptides and nucleic acids may be used as nutrients or to modulate cytokine and cell proliferation/differentiation activity and may also be involved in modulation of the immune system. The CDNA sequences, proteins their agonists and/or antagonists exhibit haematopoiesis regulating activity; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic activity; receptor/ligand activity; anti-inflammatory activity;
 Human; cytokine; cell proliferation; cell differentiation;
                           Human polynucleotide SEQ ID NO 8888.
                                                     06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                           haematopolesis activity; cadherin/tumour suppressor activity; and/or tumour inhibition activity. Included in the invention are probes represented in AAF98490 - AAF98572 which are specific for the cDNA clones
                                                                                                            AAI88828 standard; cDNA; 353 BP
                                                                                                                                                                                                                                                                                                                                      Sequence 245 BP; 85 A; 69 C; 38 G; 45 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 405; 557pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acids encoding polypeptides, useful for modulating e.g. cytokine and cell proliferation/differentiation activity, the immune system and hematopoiesis regulating activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-2000; 2000WO-US25135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200119988-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; nutrient; cytokine modulator; proliferation; differentiation; immune system modulator; tissue growth; chemotactic; demostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3' portion of cDNA encoding AS63_29 protein SEQ ID 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haematopoiesis.
                                                                                                                                                                                                                                                       290 CCTCCCTCCACTTCCTCCCATTCTCTGTGGTCCCAAAG 327
                                                                                                                                                                                                                              Local
                                                                                                                                                                        CTTGCTTCCNTCCCCCAGTGCGTTCTGTGATCGCCAAG 170
                                                                                                                                                                                                                                                                                                 3.8%;
Similarity 77.6%;
                                                                                                                                                                                                                                                                                                                                                               the secreted proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   мсСоу лм,
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treacy M,
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Bowman MR,
                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                              Score 63.4; DB 22
Pred. No. 2.4e-08;
                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collins-Racie LA,
                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>`</u>
                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agostino MJ;
                                                                                                                                                                                                                                                                                                          Length 245;
                                                                                                                                                                                                                                                                                   Indels
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gene therapy;
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AC XXX DT XX OS XXX
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AAQ12760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, the polypeptides are useful in gene therapy, activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or treatment of cancer legislations according to the content of cancer legislations according to the content of cancer legislations are content of cancer legislations are content of cancer legislations are content of cancer legislations.
                                                                Mus musculus.
                                                                                                                   T cell growth factor; AIDS; cytokine; T helper cell; ss
                                                                                                                                                                                   P40 genomic DNA.
                                                                                                                                                                                                                                          17-OCT-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                       AAQ12760 standard; DNA; 3809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 353 BP; 65 A; 59 C; 108 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 8888; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAO08897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US04927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 CTTCCCTCCCTCCACTTCCTCCCATTCTC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 3.7%;
Local Similarity 80.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTCCCTCCAGCCCGATTCCCCACATCTC 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 61.8; DB 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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0;

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Claim 1; Fig 15; 122pp; English
            Nucleic acid encoding for P40 T-cell growth factor - with AIDS or compromised immune systems, also allows prodn. of other cytokine(s).
                                                                                                                                                                                                     misc_RNA
                                                                                                                                                                                                                                  misc_RNA
                                                                                                                                                                                                                                                                                         misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
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                                                                Vansnick J,
                                                                             (RESE ) RES CORP TECHN INC.
                                                                                            08-JAN-1990;
                                                                                                           08-JAN-1991;
                                                                                                                        25-JUL-1991
                                                                                                                                     WO9110738-A.
                                                                                                                                                                         misc_RNA
                                                                                                                                                                                                                                               polyA_signal
                                                                                                                                                                                                                                                             polyA_signal
                                                                                                                                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                                                                      TATA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                 misc_signal
                                          1991-238026/32.
DB; AAR13218.
                                                                Uyttenhove
                                                                                            90US-0462158
                                                                                                          91WO-US00145
                                                                                                                                                                                                                                                         /wawel= polyd-AdC_region
/note= "Z DNA; enhancer &
3582..3588"
                                                                                                                                                                                                                                                                                                                                                                                                                 /number=
227..233
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1361..1407
                                                                                                                                                                                                                                                                                                       644..697
                                                                                                                                                                                                                                                                                                                      /note= "AP-1
589..594
                                                                                                                                                                                                                                                                                                                                               /note= "interferon regulatory factor-1 binding
    element"
                                                                                                                                                                                                                                                                                                                                                                      475..480
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2184 . . 23
                                                                                                                                                                                                     3534..3538
                                                                                                                                                                                                              /label= ATTTTA_motif
/note= " reduces sta
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/label= C-rich
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=
                                                                                                                                                            ′label≖
                                                                                                                                                                              /label= ATTTTA_motif
/note= " reduces stability of mRNA"
                                                                                                                                                                                                                          *tag=
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                                                                C,
                                                                                                                                                            ATTTTA_motif
                                                                                                                                                   reduces stability of mRNA"
                                                                                                                                                                                                            reduces stability
                                                               Simpson
                                                                                                                                                                                                                                                                                                                            binding
                     systems, also allows increased
                                                                                                                                                                                                                                                                                                                            site"
                                                                                                                                                                                                                                                                    activity"
                                                                                                                                                                                                            of mRNA"
                           for patients
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a genomic library using a murine P40 cDNA clone as a probe. The sequence, or the cDNA sequence obtd. using the sequence, can be inserted into a vector for expression of P40 in a host organism. The protein is useful for stimulating the proliferation of certain subsets of T helper cells e.g. in AIDS patients or immune
                                                                                      Claim 1; SEQ ID NO 1170; 32pp + Sequence Listing; German.
                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                   30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                         02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 1170
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See also AAQ12759 and
                                                                                                                cytosine methylation
                                                                                                                                                                                                                          (EPIG-)
                                                                                                                                                                                                                                                                                                                   03-JAN-2002
                                                                                                                                                                                                                                                                                                                                              WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                 gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL33197 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 TGTTTTCTTCCCTCCCTCCACTTCCTCCATTCTCTGT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence was obtd. from a clone,
                                                                                                                                                                     2002-130909/17.
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2000DE-1043826
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76.5%;
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Pred. No. 4.9e-07
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can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilensy

The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences

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RESULT 8
AAK70103
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Best Local S
Matches 66
31 - JAN - 2000

04 - FEB - 2000

24 - FEB - 2000

10 - MAR - 2000

11 - MAR - 2000

11 - MAR - 2000

11 - MAR - 2000

12 - MAR - 2000

13 - MAR - 2000

14 - JUN - 2000

14 - JUL - 2000

15 - JUL - 2000

16 - JUL - 2000

17 - JUL - 2000

18 - JUL - 2000

19 - JUL - 2000

11 - JUL - 2000

12 - JUL - 2000

13 - JUL - 2000

14 - JUL - 2000

14 - JUL - 2000

15 - JUL - 2000

16 - JUL - 2000

17 - JUL - 2000

18 - JUL - 2000

20 - JUL - 2000

21 - JUL - 2000

22 - JUL - 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6183 BP; 1584 A; 230 C; 1532 G; 2837 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK70103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK70103 standard; DNA; 23885 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 3.7%;
l Similarity 88.0%;
66; Conservative
2000US-0179065.
2000US-0184664.
2000US-0184664.
2000US-0189874.
2000US-0199173.
2000US-020467.
2000US-0214886.
2000US-0214886.
2000US-0214886.
2000US-021488.
2000US-0216647.
2000US-0216847.
2000US-0217496.
2000US-0218290.
2000US-0218290.
2000US-02218291.
2000US-0224519.
2000US-0224519.
2000US-0224519.
2000US-0225267.
2000US-0225267.
2000US-0225759.
2000US-02258681.
2000US-02258681.
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  23-AUG-2000
31-SEP-2000
32-SEP-2000
32-SEP
 2000US-022709
2000US-0228934
2000US-0229344
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2000US-0246524
2000US-0246524
2000US-0246610
2000US-0246611
2000US-0246611
2000US-0249208
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Best Local Similarity
                                                                                                                         Matches
23698 ATCCCTCACTTCTCTTAAGCCAA 23720
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                                                                                                                                                                                                                                                  amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703
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17-NOV-2000
17-NOV-2000
17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
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06-DEC-2000
06-DEC-2000
08-DEC-2000
08-DEC-2000
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08-DEC-2000
08-DEC-2000
                                                                                                                                                                                  Sequence 23885 BP; 6416 A; 5634 C;
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                            287 TTCCCTCCCTCCACTTCCTCCCA 309
                                                    represent sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 24915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-483426/52.
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17-NOV-2000;
                                                                                                                                                                                                        AAK87694 represent human immune/haematopoietic antigen genomic quences from the present invention. AAK54942 to AAK54950 and AAM82169 present sequences used in the exemplification of the present invention.
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                                                                                                                        Conservative
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2000US-0249297
2000US-0249299
2000US-0249390
2000US-0250160
2000US-0250391
2000US-0251988
2000US-0251988
2000US-0251479
2000US-0251479
2000US-0251856
2000US-0251868
2000US-0251868
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2000US-0254097
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2000US-0249245
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                                                                                                                3.7%; Score 60.6; DB 22; Length 23885; 83.1%; Pred. No. 2e-06; itive 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
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RESULT 9
AAK73173
26-JUL-2000;
14-AUG-2000;
12-AUG-2000;
12-AUG-2000;
12-AUG-2000;
13-AUG-2000;
13-AUG-2000;
14-AUG-2000;
14-AUG-2000;
15-AUG-2000;
16-SEP-2000;
10-SEP-2000;
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26-JUL-2000;
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07-JUL-2000;
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07-JUN-2000;
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cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK73173 standard; DNA; 23885 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001WO-US01354
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2000US-0225757.
2000US-0225758.
2000US-0225759.
2000US-0226279.
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2000US-0225268.
2000US-0225270.
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2000US-0189874.
2000US-0190076.
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2000US-0224518
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2000US-0218290
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2000US-0217487
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2000US-0216647
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2000US-0209467
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08-SEP-2000; 12-SEP-2000; 14-SEP-2000;

2000US-0232081. 2000US-0231968. 2000US-0232397. 2000US-0232398. 2000US-0232399.

2000US-0233064. 2000US-0233065. 2000US-0234223.

2000US-0232401 2000US-0233063

2000US-0234274. 2000US-0234997. 2000US-0234998. 2000US-0235484. 2000US-0235834. 2000US-02358336.

2000US-0236368 2000US-0236369

2000US-0236370

2000US-0236327 2000US-0236367

2000US-0237038

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RESULT 10
AAI90376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cattivity, and can be used in gene therapy and vaccine production. (I) CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally. (I) CC supplement the patients own production of (I). Additionally. (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC protein. (I) proteins and polynucleotides may be used to prevent, CC graces and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                               01-DEC-2000

01-DEC-2000

05-DEC-2000

05-DEC-2000

06-DEC-2000

06-DEC-2000

08-DEC-2000

08-DEC-2000

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08-DEC-2000

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01-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 27985; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23885 BP; 6416 A; 5634 C; 5563 G; 6272 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                           06-NOV-2001 (first entry)
                                                                                                                                                                        AAI90376 standard; cDNA; 415
                                                                           Human polynucleotide SEQ ID NO 10436.
                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-483426/52.
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                                                                                                                                                                                                                                                                                                                                                                             69;
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barash SC,
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0250160.
2000US-0251030.
2000US-0251030.
2000US-0251988.
2000US-0251879.
2000US-0251856.
2000US-0251868.
2000US-0251868.
2000US-0251869.
2000US-0251869.
2000US-0251869.
2000US-0251997.
2000US-0251997.
                                                                                                                                                                                                                                                                                                                                                                                              3.7%;
83.1%;
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                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               Score 60.6; DB 22;
Pred. No. 2e-06;
0; Mismatches 14;
                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Length 23885;
                                                                                                                                                                                                                                                                                                                                                                                  0;
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14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
03-OCT-2000;
03-OC

2000US-0241787. 2000US-0241808. 2000US-0241809. 2000US-0241826. 2000US-0244617. 2000US-0246474. 2000US-0246475. 2000US-0246476. 2000US-0246477.

17 NOV - 2000; 11 - NOV - 2000; 17 - NOV - 2000;

2000US-0249245. 2000US-0249264. 2000US-0249265. 2000US - 0246478.
2000US - 0246523.
2000US - 0246524.
2000US - 0246525.
2000US - 0246526.
2000US - 0246527.
2000US - 0246527.
2000US - 0246632.
2000US - 0246613.
2000US - 0246611.
2000US - 0246611.
2000US - 0249613.
2000US - 0249216.
2000US - 0249211.

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RESULT 11
AAK81626
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activino/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
      09-AUG-2001
                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                          W0200157182-A2
                                                                 cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                        07-NOV-2001 (first entry)
                                                Homo sapiens.
                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36438
                                                                                                                                                AAK81626;
                                                                                                                                                                     AAK81626 standard; DNA; 8095
                                                                                                                                                                                                                                                                                                                                                        Sequence 415 BP; 130 A; 109 C; 63 G; 112 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200164835-A2
                                                                                                                                                                                                                        243 ACACACAGAGACACACACACACACACACCTCTATTATT 284
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                                                                                                                                                                                                                                                                 nilammation
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                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                             ACACACACACACACACACACACACACACACATGTTTTCTT 288
                                                                                                                                                                                                                                                                                                                76;
                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 10436; 1399pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                        3.6%;
                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                              Score 60.4; DB 22; Length 415;
Pred. No. 2.4e-07;
D; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                differentiation or which may induce er cell populations. The useful in man them.
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  14-SEP-2000
14-SEP-2000
14-SEP-2000
21-SEP-2000
21-SEP-2000
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                                                                                                                                          18-NG-2000
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23-AUG-2000
30-AUG-2000
01-SEP-2000
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07-JUL-2000;
07-JUL-2000;
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19-MAY-2000;
07-JUN-2000;
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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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14-AUG-2000;
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2000US-0231243

2000US-0231243

2000US-0231243

2000US-02311414

2000US-0231414

2000US-0231411

2000US-0232081

2000US-0232081

2000US-0232081

2000US-0232981

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2000US-0232398

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20-OCT-2000;
20-NOV-2000;
20-NO
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             WP,I; 2001-483426/52
                                              Rosen CA,
                                                                              HUMAN GENOME SCI INC
                                              Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0241221.
2000US-0241785.
2000US-0241786.
2000US-0241787.
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2000US-0249265

2000US-0249297

2000US-0249299

2000US-0249300

2000US-0250391

2000US-025193

2000US-025193

2000US-025198

2000US-0251185

2000US-0251869

2000US-0251869

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2000US-0251869

2000US-0251869

2000US-0251989

2000US-0251989

2000US-0251989

2000US-0251989

2000US-0251999

2000US-0251997

2000US-0254097
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2000US-0240960.
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2000US-0246611.
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                                              Ruben SM
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Matches

Similarity 81.4 70; Conservative

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Indels

0;

Gaps

0

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Query Match
Best Local
                                                                                                                                                  expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis - \,
                                                                                                       Sequence 8095 BP; 2662 A; 1135 C; 1557 G; 2741 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 36438; 3071pp + Sequence Listing; English
                      3.6%;
Score 60.4; DB 22;
Pred. No. 1.3e-06;
0; Mismatches 16;
                                                   Length 8095;
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RESULT 12
AAC91904
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7247
                                                                                                                                                                         Murine; A259; integrin alpha subunit; fibrosis; liver disease; lung; kidney; cancer; osteoporosis; acute myeloid leukaemia; HIV infection; rheumatoid arthritis; ss.
                                                                                                                                                                                                                           19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                    7307 CACACACACACACACACACACACA 7332
                                                                                        mat_peptide
                                                                                                        sig_peptide
                                                                                                                                                          Mus sp.
                                                                                                                                                                                                          Murine A259 coding sequence
                                                                                                                                                                                                                                           AAC91904;
                                                                                                                                                                                                                                                           AAC91904 standard;
                                                                 WO200073339-A1.
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28..93
/*tag= b
94..3591
/*tag= c
                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                           CDNA; 4858 BP
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28-MAY-1999; 99US-0322790 27-APR-2000; 2000US-0561263

99US-0322790

15-MAY-2000; 2000WO-US13262

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the coding sequence for murine integrin alpha subunit, A259. A259 is homologous with the alphal and alphal0 integrin subunits and is overexpressed in fibrosis. A259 is implicated in regulation of proliferation, differentiation and/or function of many different cell types. Inhibitors of A259 activity are useful for the treatment of liver disease, particularly fibrosis, and also fibrosis in other organs (specifically lung and kidney). In addition, A259 can be used for treatment and prevention of cancer, osteoporosis, acute myeloid of treatment and prevention of cancer, osteoporosis, acute myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 5; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding alpha-integrin subunits, useful for treatment and diagnosis of fibrosis, e.g. of the liver \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                    Mouse, A259; integrin alpha subunit; integrin alpha 10; secreted protein; liver disease; fibrosis; lung; kidney; bone associated disorder; blood; cartilage associated disorder; haematopoietic disorder; bone marrow; ss; immune related disease; apoptotic disorder; neuronal tissue disease; neurodegenerative disease; gene therapy; cancer; cytostatic; osteopathic; nephrotropic; immunomodulator; anti-inflammatory; neuroprotective; antiarthritic; antianemic; antiallergic; antiasthmatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4858 BP; 1184 A; 1397 C; 1296 G; 981 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                        14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS16874 standard; cDNA; 4858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4518 A 4518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
                                                                    sig_peptide
                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                                                                                                          Murine A259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leukaemia, HIV infection, and rheumatoid arthritis.
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                                                                                                                                                                                                          anticonvulsant; antiparkinsonian
                                        /*tag=
94..35
                                                                    /product= "Mouse A259"
/note= "This coding sec
28..93
                                                                                                                                 28..3594
            /product= "Mature murine A259"
                                                                                                                 /*tag=
                                                                                                                                             Location/Qualifiers
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                                                                                    coding sequence is specifically claimed"
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smatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which encode secreted proteins with homology to integrin alpha subunits, gecifically to integrin alpha 10. The A259 polypeptide and nucleic acid care useful for treating liver disease or fibrosis, particularly kidney cibrosis or lung fibrosis. The A259 polypeptide and nucleic acid are also useful for diagnosing, preventing or treating cartilage and bone cassociated disorders (such as bone cancer, achondroplasia, myeloma, fibrous dysplasia, scoliasis, osteoarthritis, osteoarcoma and costeoporosis), bone marrow, blood and haematopoietic disorders (such as acute myelodid leukaemia, haemophilia, anaemia and thalassaemia), immune cautoimmune disorders e.g. AIDS, and allergic inflammatory disorders e.g. athma and psoriasis), apoptotic disorders (such as systemic lupus carthmatosus and insulin-dependent diabetes mellitus), diseases of the neuronal tissues (such as epilepsy and muscular dystrophy) and carthmatoric such as epilepsy and muscular dystrophy.
                                                                                                                                                                             ID
                                                                                                                                                                                                AAA39622
                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New A259 nucleic acids and polypeptides, which comprise integrin alpha subunit, useful for diagnosing, preventing or treating e.g. liver disease, kidney or lung fibrosis, cancers, blood disorders or immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 5; 168pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4858 BP; 1184 A; 1397 C; 1296 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related diseases
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                diagnostic;
                                                                                                         01-SEP-2000
                                                                                                                                                                                                                                                                     4518 A 4518
                                                                                                                                                                                                                                                                                                                                             4458
                                 Stomatin; murine; treatment; pain; analgesic; anesthetic;
                                                                     Murine stomatin DNA
                                                                                                                                           AAA39622;
                                                                                                                                                                               AAA39622 standard;
                                                                                                                                                                                                                                                                                                                                                                                 239
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                                                                                                                                                                                                                                                                                                                                             ACACACACACACACACACACACACACACACACACACGCACGCACCTCCCAACCATC
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                                                                                                                                                                                                                                                                                                         299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents cDNA encoding the murine A259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to human and murine A259 nucleic acid molecules
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Pred. No. 1.1e-06;
0; Mismatches 38
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                                         allodynia;
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                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel protein (I) of the stomatin family which can be used in the treatment of pain. (I) is involved in transduction of mechanical stimuli to a receptor potential, particularly in perception of pain and contact, so when the function of (I) is reduced, so will be sensitivity to pain. (I) and other members of the stomatin family, are used as target proteins for treatment of pain, and especially: (1) for the development of analgesics and anesthetics, e.g particularly for pharmaceutical development; (3) for developing diagnostic kits for predicting an individual's response to different analgesics/anesthetics or disposition to side effects, and (4) for determining disposition to disease. This sequence encodes the murine stomatin protein described in the method of the invention.
                WQ200157182-A2.
                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                      Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21626.
                                                                                                             06-NOV-2001 (first entry)
                                                                                                                                                                                                             1113 AACAACAACAACAAAACCA 1132
                                                                                                                                                                                                                                                    AAK66814 standard; DNA; 5176 BP
                                                                                                                                                                                                                                                                                                                                                                                Sequence 1787 BP; 515 A; 448 C; 426 G; 398 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 4-5; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New stomatin family protein, useful as target for developing e.g. analgesics and anesthetics, is involved in pain and contact perception
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P-PSDB; AAY87912.
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                                                                                                                                                                                                                                  353 CACACCACCATAAAAGCCCA 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-1998;
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  21-SEP-2000
21-SEP-2000
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06-SEP-2000;
08-SEP-2000;
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14-JUL-2000;
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28-JUN-2000;
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07-JUL-2000;
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05-SEP-2000;
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19-MAY-2000;
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17-MAR-2000;
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          2000US-0235834.
2000US-0235836.
2000US-0236327.
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2000US-0232401.
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2000US-0225267.
2000US-0225268.
                                        2000US-0234998.
2000US-0235484.
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2000US-0234997.
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2000US-0233065.
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2000US-0231242.
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2000US-0226868
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17-NOV-2000;
01-DEC-2000;
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05-DEC-2000;
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05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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13-OCT 2000

20-OCT 2000

01-NOV 2000

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17-NOV 2000
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17-NOV-2000;
17-NOV-2000;
                                 (HUMA-) HUMAN GENOME
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2000US-0249300
2000US-0250160
2000US-0250391
2000US-0251980
2000US-0251980
2000US-0251980
2000US-0251479
2000US-0251479
2000US-0251866
2000US-0251866
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2000US-0241786.
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2000US-0241808.
2000US-0241809.
2000US-0241826.
2000US-0244617.
2000US-0246474.
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WPI; 2001-483426/52

Rosen CA,

Barash SC,

Ruben SM;

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cc amino acid sequences given in AAM82170 to AAM81921. (1) have cytostatic contribute, and can be used in gene therapy and vaccine production. (1) crotesins and polynucleotides may be used in the prevention, diagnosis and ctreatment of diseases associated with inappropriate (1) expression. For cc example, they may be used to treat disorders associated with decreased cc expression by rectifying mutations or deletions in a patient's genome cc that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) cc polynucleotides may be used to produce the secreted (1), by inserting cc the nucleic acids into a host cell and culturing the cell to express the cc diagnose and treat immune/haematopoietic antigen genomic concers and cancer metastases of haematopoietic antigen genomic concerns terminate present invention. AAK54922 to AAK87694 represent invention. AAK54942 to AAK54950 and AAM82169 cc represent sequences sized in the example first the Concerns and cancer metastase of the concerns and cancer metastases of haematopoietic antigen genomic concerns according to the present invention. AAK54942 to AAK54950 and AAM82169
Query Match
Best Local :
                                                                       Sequence 5176 BP; 1472 A; 1210 C; 1170 G; 1324 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 21626; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                     represent sequences used in the exemplification of the present invention
                DB 22;
                Length 5176;
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Ş 밁 δã Matches 879 ACCTCTCTATCCCTTCTCT 287 TTCCCTCCCTCCACTTCCT 305 Local 3.6%; il Similarity 84.8%; 67; Conservation Score 59.8; DB 22 Pred. No. 1.5e-06; 0; Mismatches 12; Indels 0; Gaps

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Search completed: November Job time: 510.209 secs 6, 2002, 14:16:40

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Maximum Match 10
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                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: gb_ba:*

2: gb_hi:*

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4: gb_on:*

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6: gb_ph:*

8: gb_ph:*

9: gb_pr:*

11: gb_s

12: gb_s

13: gb_s

14: gb_s

15: em_
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22: em
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25: e
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Glp-2 receptor gene promoter and uses thereof

JOURNAL

14936 ONTARIO INC. (CA)

Location/Qualifiers

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14936 ONTARIO INC. (CA)

Corganism="synthetic construct"

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Lovshin,J.A., Estall,J., Yusta,B., Brown,T.J. and Drucker,D.J.
Glucagon-like Peptide (GLP)-2 Action in the Murine Central Nervous
System Is Enhanced by Elimination of GLP-1 Receptor Signaling
System 15 Enhanced by Elimination of GLP-1 Receptor Signaling
J. Biol. Chem. 276 (24), 21489-21499 (2001)
                                                                                          Direct Submission Submitted (17-JAN-2001) Department of Medicine, University of Toronto, 101 College Street CCRW3-845, Toronto, ON M5G2C4, Cai
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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KEYWORDS SOURCE ORGANISM

Mus musculus Eukaryota; Metazoa; Mammalia; Eutheria;

house mouse.

VERSION ACCESSION DEFINITION

AC016464.3 GI:7137319 HTG; HTGS_PHASE1; HTGS_DRAFT

207160 bp DNA linear Mus musculus chromosome 11 clone RP23-409J21 map 11, SEQUENCE, 21 unordered pieces.

HTG 01-MAR-2000

REFERENCE

Mus musculus chromosome Unpublished 2 (bases 1 to 207160)

Chordata; Rodentia;

Craniata; Vert Sciurognathi;

Vertebrata; Euteleostomi; Muridae;

Murinae;

REFERENCE

AUTHORS TITLE JOURNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 19648 bases at least 040
Consensus quality: 202204 bases at least 030
Consensus quality: 204082 bases at least 020
Insert size: 210000; agarose-fp
Insert size: 205160; sum-of-contigs
Quality coverage: 4.8 in 020 bases; sum-of-contigs
Quality coverage: 4.9 in 020 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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75456: contig of 11510 bp in length
75556: gap of 100 bp
8148: contig of 12592 bp in length
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                                              GCAGCCTTGAACAACACCCTGGCCTCTTTGAACCCCACTATTTCTCAGCCCTCAGATGA 952
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                                                                                                                                                                           Submitted (08-JAN-2002) Wellcome Trust Sanger Institute, Hinxton. Cambridgeshire, CBLO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 11, 2002 this sequence version replaced gi:18072579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus chromosome 11 clone RP23-338M9, *** SEQUENCING PROGRESS ***, in unordered pieces.
AL646097
                       Center project name: bM338M9
                                                               Contact: humquery@sanger.ac.uk
                                                                                                                        Center code: SC
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Assembly program: XGAP4;
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                                                                                                                                           Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                    Mclay,K
                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                       (sites)
                                                                                                     http://www.sanger.ac.uk
                                                                                                                                                                  -- Genome Center
                     Summary Statistics
                                                             Project Information
                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
    version 4.5
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                                                                                                                                                                                                                                                   /note="assembly_fragment:01439
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/chromosome="11"
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                                                                                                                                                                                                                                                                                                                                                             Db 133482 CACCACCATAAAAGCCCATCTGGGAGCCATTTCCAGACTGATCTTTTTATCATTAAGGTT 133423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 133722 ATTTCAAGAAGCAAGATGGAATATTTGTACAAAACAGGTGCTTTCTCCCCCACCATGCGA 133663
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953 AGAAGTAATGGTACCTTGGAGGATACTGATGGGTTCAAGTGAACTAGGGCAGAGGGTGGA 1012
                                                                                                                                                             355 CACCACCATAAAAGCCCCATCTGGGAGCCATTTCCAGACTGATCTTTTTATCATTAAGGTT 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                   CAGGTAGCTGTGGTCACGTGACTCGGCTGGAAGSCCTGGCTTTGTCTTTTTTGCTTGCTGT 892
                                                                                                                                                                                         CTGCTTCCCTGTGAATGTTCAGAATTCACTGGGCTTGGTCAGCTAATGGAAATGATCTAT 534
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Sequence 6 from Patent WO0179290.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                   /organism="Mus sp."
/db_xref="taxon:10095"
/protein_id="CAD22992.1"
/db_xref="GI:18619544"
                                                                   /codon_start=1
                                                                                                   /note="unnamed protein product"
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KEYWORDS
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                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Locus
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1474 ATGTCTTGCTTTTCTTGGGCTTGCTGAGGAAGTCCCAGGCAGCGTAGACGTCTTGGG 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1594 GGAGATTCGGTAGATCGCTGTAGAGCAACTCAGACAGTCGGCGGCCTGAAGAGGACTTGT 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1534 GGTAGGTCTGGGAAAAATCTCCCCAAGATTTTAGGAGGGGCAGGCGGGGGATGAGAAACTT 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1654 GCAAACA 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Graham, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Graham, J., Grant, G., Hagos, B., Heaford, A., Horton, L., Graham, J., Lancoque, K., Lamazares, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McGrithy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McIdrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Fesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Ye, W.J., Vossiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Pisani, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAAACA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                   submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 26, 2001 this sequence version replaced gi:14547870. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boguslavkly, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 198271)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACO26591 198271 bp DNA linear Homo sapiens chromosome 17 clone RP11-655D3 map 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 17, clone RP11-655D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC026591.9 GI:15291083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN PROGRESS ***, 4 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 198271)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 a
                                          Center: Whitehead Institute/ MIT Center for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MRRLWGPGTPFLSLLLLVSIKQ"
132 c 155 g 104 t 2 ot
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                                                                                 Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 175; DB 6; Pred. No. 5.7e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 493;
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**G

27-AUG-2001 SEQUENCING

Research

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Db 145200 ACAAAACCAAAAACGAAGTGAAAACATGTTCTTCTTGCCTCTTGCTGACTCACTGTTCCA 145141
                                                                                                                                                                                                                         Db 145298 CTGCTTTTCCCCAACTGTTCAGAATTCAGTTGAAAAGTTACCCAGGATGAGTTCCTA 145239
                                                                                                                                                                                                                                                                                                                                 Db 145358 TAAAATCTTGTCACATGGAGTTTTTAAGATTTTTAGGGATGTCTATTAAGAAAAGCATGG 145299
                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 145418 CACCACTCTGAGTCCATTTCTAGGGTCTTTGTTCTAGTTGAGCTTTTCATTGTTAAGGTC 145359
                                                                                                                   Db 145238 TGTTTGACTTGAAGAGGAAGGAAAAAATA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 145533 AGTTGCAGCCACATTCAATGAC-----CAAAGTCCATCCCTTGGGTACTTTCTCCCTCTG 145479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 145589 ACCATTTTCCAGC----ATGCAACTTGGAAGATGATCTTTAATGAGCACTCACAGAACGG 145534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 145649 AAAAGTTGCAAGAGATGAGATGGAATATTCTTGCAAAGCAGGTATTTTCTTTAAAGACAG 145590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.1%;
Best Local Similarity 49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 AAGCATTTCAAGAAGCAAGATGGAATATTTGTACAAAACAGGTGCTTTCTCCCCCCACCAT 174
                                                    595 GGGAAGGGAAAACTGCCTTTTATGCCTATTGCTACTCTAACATTTTGTCTCTCACCTTCC 654
                                                                                                                                             475 CTGCTTCCCTGTGAATGTTCAGAATTCACTGGGCTTGGTCAGCTAATGGAAATGATCTAT 534
                                                                                                                                                                                                                                                                                                                                                                    415 TGAATTCTTGCCACGTGTGGGTTTTAAGGTTTTTAAGGGATTTTTATCTAGCGGCACTCAC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 CACCACCATAAAAGCCCATCTGGGAGCCATTTCCAGACCTGATCTTTTATCATTAAGGTT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 GCGACCCGGGAGCTCCACTGATATGGACAGAATAGCTTTACAGCTACATTCAAAACACAC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 153566: contig of 153566 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52858 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153567 153666: gap of 100 bp
153667 158888: contig of 5222 bp in length
158889 158988: gap of 100 bp
158989 189474: contig of 30486 bp in length
189475 189574: gap of 100 bp
189575 198271: contig of 8697 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ project Information
Center project name: L8450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: 655_D_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="RP11-655D3"
/clone_lib="RPCI-11 Human Male BAC"
/45543 c 46237 g 53270 t 363 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="17"
/map="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .198271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 101.6; DB 2; Length 198271; Pred. No. 1.9e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 696; Indels 125; Gaps
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| Qy 1655 CAAACA 1660 |
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| QY 1599 TTCGGTAGATCGCTGTAGAGCAACTCAGACAGTCGGCGGCCTGAAGAGGGACTTGTG 1654 |
| Qy 1554 CCCAAGATTTTAGGAGGGGCAGGCGGGGGATGAGAAACTTGGAGA 1598 |
| QY 1494 GGCTTGCTGAGGAAGTCCCAGGCAGCCTAGACGTCTTGGGGGTAGGTCTGGGAAAAATCT 1553 |
| Qy 1448AGAATAGAATCCTCGGAATGGTAACCATGTCTTGCTTTTCTTCTG 1493 . |
| QY 1409 CTCTCCAGCCATCCGAATCTCAATCTGGTCGTGTGCGTA |
| 33 T |
| OY 1299 AGTAACCACGGAGCTCTGAGATAGCCCTGAGCTGGTGCCGTTTAGAAAAGTT 1350 |
| QY 1239 CTGGGGTCTGGAGGTGTTGTCTCTGAGACAGGAAAACTCATCTTGTTACTATGGCATAGT 1298 |
| QY 1179 GTTTTGTTACCGTGTAAACGCAACTCAACTCTCGGCACTGAACAGGCTTTTGCTGCAGAC 1238 |
| QY 1119 CGGCCCACTCAGAACACGGGGACAATTGAAAGGCACCAACCTCCGTGCTTCCTACCCGTT 1178 |
| QY 1059 CCATGAATACCATAAAAATATCTGTCAGGTGGCCAGAGCATCACTGTGTTCAGAACACAA 1118 |
| QY 999 GGGCAGAGGGTGGAAGGTTTTGTAACCATAAACTGAAGTGGGGTGTTGGTTAGTAAGTA |
| QY 940 AGCCCTCAGATGAAGAAGTAATGGTA-CCTTGGAGGATACTGATGGGTTCAAGTGAACTA 998 |
| QY 880 TTTTGCTTGCAGCCTTGAACAACACCCTGGCCTCTTTGAACCCCACTATTTCTC 939 |
| QY 828 CTAACCAGGTAGCTGTGGTCACGTGACTCGGCTGGAAGSCCTGGCTTTGTCT 879 |
| QY 775 TGCTAGAGAYCATGAGCTTYCTTTGAGACCCCTAGTGCTAACAGGAATAGTTC 827 |
| Qy 715 GTGTGTGTGTGGGGGGGGGGGGGGGAGCAAGCAGAGCCTTAGAGACAGAGAAAGAGCC 774 |
| QY 655 ACTTGGTTCTTCAATGGAAAGACTGGATAGAAAGCTGGGAGCCAGCC |

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Db 144074 CAAACA 144069
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REFERENCE
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ORGANISM
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TITLE
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O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Milson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zalnoun,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; Homi
1 (bases 1 to 210719)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, 12 unordered pieces. AC087646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Research, 320 Charles Street, Cambridge, MA 02141, USA On May 31, 2001 this sequence version replaced gi:13493095. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Homo sapiens chromosome 17 clone RP11-773021 map 17, WORKING DRAFT
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* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 17, clone RP11-773021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zembek,L., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                                                                                                                      Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 205962 bases at least Q40 Consensus quality: 208431 bases at least Q30 Consensus quality: 2080431 bases at least Q30 Consensus quality: 208049 bases at least Q30 Insert size: 205000; agarose-fp Insert size: 205019; sum-of-contigs
                                                                                                                                                                                                                                            Quality coverage: 8.4 in Q20 bases;
Quality coverage: 8.2 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: 773_0_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: L11995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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sum-of-contigs
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                                                                                                             Query Match
                                                                           Matches 803;
73808 AAAAGTTGCAAGAGATGAGATGTGTTGTTGCAAAGCAGGTATTTTCTTTAAAGACAG 73749
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                                   115 AAGCATTTCAAGAAGCAAGATGGAATATTTGTACAAAACAGGTGCTTTCTCCCCCACCAT 174
                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved
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89702 10500
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75355 76881; contig of 1527 bp in length
76882 76981; gap of 100 bp
76982 78538; contig of 1557 bp in length
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                                                                           Conservative
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121202. .154071
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/clone_lib="RPCI-11 Human Male BAC"
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                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment"
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47911 c 46884 g
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                                                                                             6.18;
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105000: contig of 15299 bp in length
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210719: contig of 16634 bp in length
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89601: contig of 3192 bp in length
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82098: contig of 2052 bp in length
198: gap of 100 bp
86309: contig of 4111 bp in length
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contig of 1308 bp in length
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72767 GTTTTGCTATTGTGTAGGCATAACCTA-----CGCCGCTGATTGGGTTTTTGCTTCATGG 72713
                                                                                       72827 ACATGTGCTTAGAACAAGTGGGCATTCAAGATGAGTGAATGTTGCACTTTTCAACACACT
                                                                                                                                                                             72887 GCTGGTTAGTAAGTGATGTATCATCAATTCCATAAAAGGGTCTGTCAGGTGGGCTGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73183 GAGGCATGGCGATGAGCCTGCTAAGAACTCACCGGAGAGGGCAGGGGCAGGACAGGCCAC 73124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73239 ACGCTGGGAGCTGGCCTGGGAGAGGTGGAGTAAGAAGTTCC----AAGCAGAGCCTTTGG 73184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73359 ACAAAACCAAAAACGAAGTGAAAACATGTTCTTCTTGCCTCTTGCTGACTCACTGTTCCA 73300
                                         1179 GTTTTGTTACCGTGTAAACGCAACTCAACTCTCGGCACTGAACAGGCTTTTGCTGCAGAC 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCATGAATACCATAAAAATATCTGTCAGGTGGCCAGAGCATCACTGTGTTCAGAACACAA 1118
                                                                                                                                                                                                                                                                GGATGGTGGGTTAAAAGACGT----TGTCAATGTGAGTTGTGGGGGACAGCCTACTCCTGT 72888
                                                                                                                                                                                                                                                                                                                                                      AGCTGTCAAATGGAGAATTCATCGTATCCTCATGGGGTTATTGTCAGGATGTGCGAAATA 72944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTGCTTGCTGTGCAGCCTTGAACAACACCCTGGCCTCTTTGAACCCCCACTATTTCTC 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTCCCAAGTACCTGTGCTCAAGCAACTCTGGTCAGAAGACCTGCCTATCCGGTTCTGCT 73064
                                                                                                                                 CGGCCCACTCAGAACACGCGGACAATTGAAAGGCACCAACCTCCGTGCTTCCTACCCGTT 1178
                                                                                                                                                                                                                                                                                                                                                                                  AGCCCTCAGATGAAGAAGTAATGGTA-CCTTGGAGGATACTGATGGGTTCAAGTGAACTA 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTAACCAGGTAGCTGTGGTCACGTGACTCGGCTGGAAGSCCTGGC------TTTGTCT 879
                                                                                                                                                                                                                                                                                                              GTTTACTTGCTGTGTGGCTTTGGGCAAGCCATCCAACCTCTCTGAGCCTCAATGTTTCTC 73004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGAAGGGAAAACTGCCTTTTATGCCTATTGCTACTCTAACATTTTGTCTCTCACCTTCC 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCATTTTCCAGC----ATGCAACTTGGAAGATGATCTTTAATGAGCACTCACAGAACGG 73693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAAATCTTGTCACATGGAGTTTTTAAGATTTTTAGGGATGTCTATTAAGAAAAGCATGG 73458
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                 Sequencing vector: M13, 100%
Sequencing vector: M13, 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of
                                                                                                                                  Assembly program: Phrap; version 0.990319
                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                         MO 63108, USA
On Dec 11, 20
                                                                                                                                                                                                                                                                                                                                                   Submitted (16-MAY-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 213359)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 213359)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC069006 213359 bp DNA linear HTG 11-DEC-2000 Homo sapiens chromosome RPCI-11 clone RP11-773021, WORKING DRAFT SEQUENCE, 16 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                    2000 this sequence version replaced gi:9280811
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                        0% of reads
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Insert size: 211859; sum-of-contigs
Quality coverage: 5.34 in Q20 bases; agarose-fp
Quality coverage: 5.44 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 203603 bases at least Q40 Consensus quality: 206822 bases at least Q30 Consensus quality: 208592 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                     /note="assembly_name:Contig25"
40515. .53087
                                                                                             vector_side:right"
24763. .32389
                                                                                                                                   clone_end:T7
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4722. .7894
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                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
 /note="assembly_name:Contig26"
                                                                         /note="assembly_name:Contig24"
                                                                                                                                                                        16919
                                                                                                                                                                                                                                                               /note="assembly_name:Contig20"
                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="RPCI-11"
                                                                                                                                                                                      note="assembly_name:Contig22"
                                                                                                                                                                                                                         note="assembly_name:Contig21"
                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-773021"
                                                                                                                                                                                                                                              .10806
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                                                          .40414
                                                                                                                                                                        . 24662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of unknown length contig of 25957 bp in length gap of unknown length contig of 27557 bp in length gap of unknown length
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contig of 7925 bp ir
gap of unknown lengt
contig of 12573 bp
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contig of 3121 bp in
gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of unknown length contig of 22715 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of unknown contig of 2812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig of 3173 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of unknown length contig of 16011 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of unknown length contig of 11489 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of unknown contig of 5912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 42083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 7627
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                     828
                                                                                                                                                                                                                                                                                                                                                                                             535
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CTAACCAGGTAGCTGTGGTCACGTGACTCGGCTGGAAGSCCTGGC-----TTTGTCT 879
                                                          GAGGCATGGCGATGAGCCTGCTAAGAACTCACCGGAGAGGGCAGGGGCAGGACAGGGCAC 84363
                                                                                                                                                                                                                                                                                                                    GGGAAGGGAAAACTGCCTTTTATGCCTATTGCTACTCTAACATTTTGTCTCTCACCTTCC 654
                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCTTTTCCCAACTGTTCAGAATTCATTCAGTTGAAAAGTTACCCAGGATGAGTTCCTA 84637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAAATCTTGTCACATGGAGTTTTTAAGATTTTTAGGGATGTCTATTAAGAAAAGCATGG 84697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGAATTCTTGCCACGTGTGGGTTTTTAAGGTTTTTTAGGGATTTTTATCTAGCGGCACTCAC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCACTCTGAGTCCATTTCTAGGGTCTTTGTTCTAGTTGAGCTTTTCATTGTTAAGGTC 84757
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                                                                                                                                 ACGCTGGGAGCTGGCCTGGGAGAGGTGGAGTAAGAAGTTCC----AAGCAGAGCCTTTGG 84423
                                                                                                                                                                    GTGTGTGTGTGTGGGGGGGGGGGGGCAGCAGCAGAGCCTTAGAGACAGAGAAGAGCC
                                                                                                                                                                                                                                                                                 ACAAAAACCAAAAACGAAGTGAAAACATGTTCTTCTTGCCTCTTGCTGACTCACTGTTCCA 84539
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                                                                                                                                                                                                         ACCAATCAAGACATCTTCCACCTGGGCCTCCAATTTGGGAGGCTGGGAGACATTGCAGGG 84479
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                                                                                             rgctagagaycargagctryctrtgagacccctagtgctaacaggaata-----gtrc 827
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171277, .213359
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/note="assembly_name:Contig31
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64777. .78536
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117563. .143519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACATGTGCTTAGAACAAGTGGGCATTCAAGATGAGTGAATGTTGCACTTTTCAACACACT 84007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCCTGCTTTTGGGGGGGGGAGGGGGGGGGGGGATGAGCCCAGGGCCGAGAAGGAACTCTGAAG 83533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCGTGCATTGAGCAGAACCTTCAGGGTGGAGCCCGCTTGACCGCCTTGTTCTTCTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGGGCTGGGAGCTGTTCTCCTGAGCTGAGCAACCACCTCTCCTGCAGTCTCTGCAT 83892
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                                                                                                                                                                                                                                SEQUENCE SAMPLING AC100859
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                Homo sapiens
                                                                                                                                                                    AC100859.1 GI:17048229
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                                                                                                             HTGS_PHASEO
                                                                                                                                                                                                                                                                                                                                   clone RP11-615H7 map 15,
                                                                                                                                                                                                                                                                                                                                                                               DNA
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LOW-PASS
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TITLE
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 15, clone RP11-615H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996–1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be preserved.
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14588 14687; gap of 100 bp 11 length 15513 15512; gap of 100 bp 16180 16279; contig of 667 bp in length 15513 16179; contig of 667 bp in length 16280 16529; gap of 100 bp 1655 bp 16565 17064; gap of 100 bp 17065 17785; contig of 685 bp in length 17786 17885; gap of 100 bp 17786 17885; gap of 100 bp 18618 18717; gap of 1725 bp in length 18618 18717; gap of 1726 bp in length 18718 19443; contig of 732 bp in length 18718 19443; contig of 736 bp in length 18718 19544 19543; gap of 100 bp 19544 19543; gap of 100 bp 19544 19543; contig of 736 bp in length 20280 20379; gap of 100 bp 21116 21215; gap of 100 bp 21116 21215; gap of 100 bp 100 bp 2116 21215; gap of 100 bp 100 bp 2116 21215; gap of 100 bp 100 bp 2116 21215; gap of 100 bp 100 bp 21216 21215; gap of 100 bp 10
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26181 26880; contig of 732 bp in length
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29418 30119; contig of 698 bp in length
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30120 30926; contig of 707 bp in length
30120 30926; contig of 707 bp in length
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22070 2774; contig of 705 bp in length

22175 22874; gap of 100 bp

22875 23595; contig of 721 bp in length

23596 23695; gap of 100 bp

23696 24428; contig of 733 bp in length

24429 24528; gap of 100 bp

24529 25248; contig of 730 bp in length
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10567 11291: contig of 725 bp in length
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9650 9749: gap of 100 bp
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13762: contig of 747 bp in length
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12133: contig of 742 bp in length
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14587: contig of 725 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23907 GTTCAGAATTCATTCAGTTGAAAAGTTACCCAGGATGAGTTCCTATGTTTGACTTGAAGA 23966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      490 TGTTCAGAATTCACTGGGCTTGGTCAGCTAATGGAAATGATCTATGGTTTGACTTAAATG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 TGTGGGTTTTAAGGTTTTTAGGGATTTTTATCTAGCGGCACTCACCTGCTTCCCTGTGAA 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                      550 TGAAAGGAAAAAAA 564
                                                     102783 bp D
Rattus norvegicus clone CH230-11B19,
***, 51 unordered pieces.
AC096120
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                            AC096120.3 GI:17943804
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37617 38346: contig of 730 bp in length
38347 38446: gap of 100 bp
38447 39150: contig of 704 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39914 40013: gap of 100 b
40014 40761: contig of 710
40762 4076
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/db_xref="taxon:9606"
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48857: contig of 756 bp in length
957: gap of 100 bp
49665: contig of 708 bp in length.
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Pred. No. 3.7e-12;
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AUTHORS
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TITLE
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Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:16901736.
                                                                                                                                                                                                                                                                                                                                                                                  findPhrapList
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Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Consensus quality: 92140 bases at least Q40 Consensus quality: 98027 bases at least Q30 Consensus quality: 102801 bases at least Q30 Estimated insert size: 79332; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: CH230-11B19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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* NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 51 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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Best Local Similarity
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ORGANISM
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                                               Rattus norvegicus clone CH230-9C13, 64 unordered pieces.
Rattus norvegicus
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                                AC095179.2 GI:17942259
            Norway rat.
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    102783
/organism="Rattus norvegicus"
/db_xref="taxon:10116"

                                                                                                                                                                                                                                                                                                                                                /clone="CH230-11B19"
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100542: contig of 1168 b
100642: gap of unknown l
101651: contig of 1009 b
101751: gap of unknown l
102783: contig of 1032 b
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95621: contig of 1247 1
95721: gap of unknown 1
96844: contig of 1123 b
96944: gap of unknown 1
98084: contig of 1140 b
98184: gap of unknown 1
98274: contig of 1090 b
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Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Coyle, M.D., Dathorne, S.R., Dathaney, K.R., Delgado, O.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgal, D., Edwards, C.C.,
Parker C., Coyle, M. Falle, M., Farrantto, D., Garden, M., Ford, J.,
Parker C., Coyle, M., Carlon, M., Carron, M., Carlon, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15625733.
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Elhaj, C., Escotto, M., Falls.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
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* NOTE: Estimated insert size may differ from sequence length 
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) 
* NOTE: This is a 'working draft' sequence. It currently
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                                                                                                                                                                                                                                            Consensus quality: 147096 bases at least Q40 Consensus quality: 154402 bases at least Q30 Consensus quality: 160566 bases at least Q20 Estimated insert size: 145980; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Assembly program: Phrap; version 0.990329First call to
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                                                                                                                                                                                                                                                                             sum-of-contigs estimation
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consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grande, S., Goyette, M., Grande, S., Goyette, M., Grande, Grande, Grande, G., Grande
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be preserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 bp 100 to 2374; contig of 728 bp in length 2474; gap of 100 bp 100 bp 3195; contig of 77.
                                      100 bp 1 length 6520: contig of 726 bp in length 6620: gap of 100 bp 7350: contin ~ f 7350:
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1546: contig of 718 bp in length
1646: gap of 100 bp
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                      7450:
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866: contig of 733 bp in
gap of 100 hr
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of 728 bp in length
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16383 16482: gap of 100 bp
16483 17202: contig of 730 bp in length
17202 17301: gap of 100 bp
17302 18013: contig of 712 bp in length
18114 18113: gap of 100 bp
18114 1813: gap of 100 bp
18114 18926: contig of 713 bp in length
18927 18926: gap of 100 bp
19949 19748: gap of 100 bp
19949 20470: contig of 722 bp in length
19749 20470: contig of 772 bp in length
19749 20470: contig of 720 bp
19749 20470: contig of 720 bp
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25396 25495: gap of 100 bp
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35131: gap of 100 bp
5231: gap of 727 bp
35958: contig of 727 bp
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27854: contig of 719 bp
7954: gap of 100 bp
28664: contig of 710 bp
8764: gap of 100 bp
29468: contig of 704 bp
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068: gap of
9775:
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375: contig of 707 L
10583: contig of 708 hr
10583: gap of
11307
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33517: contig of 6
617: gap of 10
34307: contig of 6
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30300: contig of 732 bp
100: gap of 100 bp
31134: contig of 734 bp
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32798: contig of
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31970: contig of 736 b
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26207: contig of 712 b
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                                             378 GAGCCATTTCCAGACTGATCTTTTTA 403
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                                                                                                                                                                                                                   h 4.3%; Score 72.2; DB 2; Length 72930; Similarity 40.2%; Pred. No. 1.5e-10;
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40186 40918; contig of 733 bp in length
40919 41018; gap of 100 bp
41019 41750; contig of 732 bp in length
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38422 38521: gap of 100 bp
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50858 51575; contig of 718 bp in length
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48396 49105; contig of 710 bp in length
49106 49205; gap of 100 bp
49206 49927; contig of 722 bp in length
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46779 47492: contig of 714 bp in length
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42674 43404: contig of 731 bp in length
43405 43504: gap of 100 bp
43505 44224: contig of 720 bp in length
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56478: contig of 711 bp in length
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55667: contig of 717 bp in length
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48295: contig of 703 bp in length
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53225: contig of 715 bp in length
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45038: contig of 714 bp in length
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45852: contig of 714 bp in length
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Best Local Similarity 67.6%;
                                                                                                                                                                                                                                     AUTHORS
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                 Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Bydd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-SEP-2001) Graduate Institute of Basic Medical Sciences, Chang-Gun University School of Medicine, 259 Wen-Road, Kwei-Shan, Tao-Yuan, Taiwan 033, Republic of China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus strain 129/SvJ chromosome 6 map 6F1-F2 sequence AF417202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus clone CH230-189013, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee, C.-M. and Chang, Y.-S.
129/SvJ mouse genomic clone
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                                                                                                                                                                                                        Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1.
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Lee, C.-M. and Chang, Y.-S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C
                                                                                                                                                                                                                                                                                                                                                                              Norway rat
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                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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JOURNAL REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             findPhrapList
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On Dec 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 42 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                       be preserved
                                                                                                                                                                                                                                                                                                                                                                                                   Consensus quality: 151055 bases at least Q40 Consensus quality: 158732 bases at least Q30 Consensus quality: 165129 bases at least Q30 Estimated insert size: 160905; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation quality coverage: 2.5x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: GGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: hgsc-help@bcm.tmc.edu
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                      12798: contig of 12898: gap of 125227: contig of 25327: gap of 137905: contig of 37905: gap of 45387: contig of
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                                                                                                                                                             Cople, L., Chowdonfy, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Davy-Carroll, L., Dederich, D.A., Douthwalte, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevard, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Harti, M., Havlak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hamilton, E., Jacobson, B., Jla, Y., Johnson, R., Johlvet, S., Jackson, L.E., Jacobson, B., Jla, Y., Johnson, R., Johlvet, S., Jackson, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lewis, L.C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lij, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Moguen, N., Noterson, E., Nokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Perez, L., Peters, L., Pickers, R., Primus, E., Pu, L.L., Peters, L., Pickers, R., Primus, E., Pu, L.L., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanlev, H., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanlev, H.,
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Rattus norvegicus clone CH230-8E8, *** SEQUENCING IN PROGRESS ***
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatck,A., Tabor,P., Tamerisa,A., Tamerisa,A., Tangy,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,F wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Norway rat.
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/db_xref="taxon:10116"
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                                                     Vinson, R.
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15627273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 59 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 184550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 148944 bases at least Q40 Consensus quality: 156886 bases at least Q30 Consensus quality: 162839 bases at least Q20 Estimated insert size: 155616; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-----Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: Phrap; version 0.990329First call to
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119325: gap of unknown |
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125146: contig of 2590 |
125246: gap of unknown |
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13789: contig of 1718 |
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Search completed: November Job time: 4880.42 secs
                                                                                                                     Db 152002 CTTCATGCTCACGCCCTTGTCTCTGGGTCTCTGGGGCCAGAGAGA 151958
                                                                                                                                                                                        Query Match
Best Local S
Matches 82
                                                                                       286 CTTCCCTCCACTTCCTCCCATTCTCTGTGGTCCCAAAGAGA 330
                                                                                                                                                                                        1 Similarity 78.1
82; Conservative
                                                                                                                                                                                                                                                   176669
178014
178114
179640
179740
180773
                                                                                                                                                                                                                                              178013: contig of 1345 bp in length 178113: gap of unknown length 179639: contig of 1526 bp in length 179739: gap of unknown length 180772: contig of 1033 bp in length 180872: gap of unknown length
                                                                                                                                                                                                     4.18;
              6,
              2002, 17:33:11

 Mismatches

                                                                                                                                                                                                     Score 68.2; DB 2; Length 184550; Pred. No. 2.6e-09;
                                                                                                                                                                                      Indels
                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                    0;
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